

52552

From: Chan, Christina
Sent: Tuesday, October 09, 2001 12:52 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/580523

Please rush. Thanks Chris

-----Original Message-----

From: Davis, Minh-Tam
Sent: Tuesday, October 09, 2001 12:37 PM
T : Chan, Christina
Subject: Rush search request for 09/580523

*priority date 05/99
2000*

Please search in commercial data base and issued patent file:

- 1) SEQ ID NO:1
- 2) SEQ ID NO:1, without Serine, or glycine or alanine at amino acid position 118.
- 3) SEQ ID NO:1 having alanine at amino acid position 118.
- 4) Amino acid sequence 103-123 of SEQ ID NO:1.
- 5) An amino acid sequence comprising the amino acid sequence 143-168 of SEQ ID NO:1, but no serine at amino acid position 118.
- 6) Please search SEQ ID NO:1 against the parent case 60/136783 for priority date.

Thank you

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

Point of Contact:
Jan Delavel
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Point of Contact:
Jan Delaval
Librarian-Physical Sciences
CM1 1E01 Tel: 308-4498

STAFF USE ONLY

Searcher Jan
Searcher Phone # 4498
Searcher Location _____
Date Searcher Picked Up 10/9
Date Completed 10/9
Searcher Prep & Review Time _____
Clencal Prep Time 20
Online Time 30

Type of Search

NA Sequence (#) _____
AA Sequence (#) 5
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
Dialog _____
Questel/Orbit _____
Dr Link _____
Lexis/Nexis _____
Sequence Systems ☒ _____
WWW/Internet _____
Other (specify) _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:52:36 ; Search time 25.99 Seconds
(without alignments)
20.598 Million cell updates/sec

Title: US-09-580-523-l_COPY_143_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWMDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	145	100.0	168	3	US-08-985-335-1
3	145	100.0	168	3	US-08-985-335-7
4	139	95.9	166	1	US-08-665-617-2
5	120	82.8	204	1	US-08-333-565-2
6	120	82.8	204	2	US-08-661-479-2
7	120	82.8	204	2	US-08-733-505A-1
8	120	82.8	204	2	US-08-733-505A-12
9	120	82.8	204	2	US-08-733-505A-13
10	120	82.8	204	2	US-08-733-505A-14
11	120	82.8	204	2	US-08-717-123-3
12	84	57.9	16	1	US-08-333-565-17
13	84	57.9	16	2	US-08-661-479-17
14	81	55.9	16	1	US-08-333-565-28
15	81	55.9	16	2	US-08-661-479-28
16	55	37.9	9	2	US-08-733-505A-44
17	50	34.5	138	2	US-07-857-224B-112
18	50	34.5	151	1	US-08-614-935-28
19	50	34.5	151	3	US-09-130-287-20
20	50	34.5	1170	1	US-08-313-288B-20
21	49	33.8	137	2	US-07-857-224B-110
22	47	32.4	492	4	US-09-342-749-2
23	46	31.7	18	1	US-08-029-333-16
24	46	31.7	30	1	US-08-029-333-15
25	46	31.7	30	1	US-08-347-000-8
26	46	31.7	219	2	US-08-796-676-1
27	46	31.7	855	2	US-08-482-090-12

28 46 31.7 856 2 US-08-481-700B-8 Sequence 8, Appli
29 46 31.7 856 2 US-09-007-383-16 Sequence 16, Appli
30 45 31.0 863 1 US-08-325-547-4 Sequence 4, Appli
31 45 31.0 869 1 US-08-188-582-32 Sequence 32, Appli
32 45 31.0 869 1 US-08-646-715-32 Sequence 32, Appli
33 44 30.3 9 2 US-08-706-741B-79 Sequence 79, Appli
34 44 30.3 9 2 US-08-924-695A-79 Sequence 111, Appl
35 44 30.3 137 2 US-07-857-224B-111 Sequence 29, Appl
36 44 30.3 150 1 US-08-614-935-29 Sequence 29, Appl
37 44 30.3 150 3 US-09-130-287-20 Sequence 29, Appl
38 44 30.3 390 2 US-08-614-156B-1 Sequence 1, Appli
39 43 29.7 162 1 US-08-087-016-4 Sequence 5, Appli
40 43 29.7 890 1 US-08-145-006C-5 Sequence 5, Appli
41 43 29.7 890 5 PCT-US94-00545-5 Patent No. 5516630
42 43 29.7 1091 6 5516630-2 Sequence 6, Appli
43 43 29.7 1528 1 US-08-463-092B-6 Sequence 6, Appli
44 43 29.7 1528 2 US-08-462-109A-6 Sequence 6, Appli
45 43 29.7 1528 2 US-08-460-907B-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match 100.0%; Score 145; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.6e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWMDRNLGRGSSAPSQ 26

DB 143 QSSSWTRVFQSWMDRNLGRGSSAPSQ 168

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? MEDIUM TYPE: IBM PC compatible
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? OPERATING SYSTEM: PC-DOS/MS-DOS
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? SOFTWARE: PatentIn Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
?
? APPLICATION NUMBER: US/08/665,617
?
? FILING DATE:
?
? CLASSIFICATION: 530
?
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Saliwanchik, David R.
?
? REGISTRATION NUMBER: 31,794
?

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REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-617-2

Query Match 95.9%; Score 139; DB 1; Length 166;
Best Local Similarity 92.3%; Pred. No. 2.7e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
Db 141 QSSWTRVFQSWDRNLGRGTAAPSQ 166

RESULT 5
US-08-333-565-2
Sequence 2, Application US/083333565
Patent No. 5622852

GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
of mouse BAD."

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Best Local Similarity 73.1%; Pred. No. 2.1e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
Db 179 QSAGWTRIIQSWDRNLKGGSTPSQ 204

RESULT 6
US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
of mouse BAD."

Query Match 82.8%; Score 120; DB 2; Length 204;
Best Local Similarity 73.1%; Pred. No. 2.1e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
Db 179 QSAGWTRIIQSWDRNLKGGSTPSQ 204

RESULT 7
US-08-733-505A-1
Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

RESULT 10

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RESULT 11
US-08-717-123-3
; Sequence 3, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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Best Local Similarity 73.1%; Pred. NO. 2.1e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Query Match 57.9%; Score 84; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. NO. 2.1e-06;
Matches 12; Conservative 2; Mismatches 1; Indels

QY 5 WTRVFQSWDRNLGR 19
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Db 2 WTRIQSWDRNLGK 16

RESULT 13
US-08-661-479-17
; Sequence 17, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-17

Query Match 57.9%; Score 84; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.1e-06;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 WTRVFQSWDRNLGR 19
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Db 2 WTRIQSWDRNLGK 16

RESULT 14
US-08-333-565-28
; Sequence 28, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-28

Query Match 55.9%; Score 81; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.9e-06;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNL 17
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Db 1 SAGWTRIQSWDRNL 16

RESULT 15
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; Sequence 28, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-28

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-28

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Query Match      55.9%; Score 81; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.9e-06;
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Db 1 SAGWTRIIQSWDRNL 16

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Search completed: October 9, 2001, 15:52:36
Job time: 151 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 16:08:31 ; Search time 36.31 Seconds
(without alignments)
33.961 Million cell updates/sec

Title: US-09-580-523-1_COPY_143_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table:

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Total number of hits satisfying chosen parameters: 311045

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	120	82.8	204	5	US-09-922-378-3
3	115	79.3	201	1	PCT-US01-18569-2762
4	52	35.9	66	1	PCT-US01-08631-56706
5	52	35.9	103	5	US-09-617-681A-7103
6	50	34.5	97	1	PCT-US01-08631-58580
7	50	34.5	140	5	US-09-758-446-1130
8	50	34.5	257	1	PCT-US01-08631-37015
9	50	34.5	1170	5	US-09-784-356-114
10	50	34.5	1223	5	US-09-758-447-658
11	49	33.8	37	5	US-09-764-905-10865
12	49	33.8	168	1	PCT-US01-08631-37014
13	49	33.8	458	1	PCT-US01-14827-9450
14	49	33.8	1189	1	PCT-US01-08656-8991
15	48.5	33.4	209	1	PCT-US01-08656-7468
16	48.5	33.4	241	5	US-09-803-110-12532
17	48	33.1	93	1	PCT-US01-08631-47656
18	48	33.1	127	5	US-09-649-866A-1103
19	48	33.1	139	5	US-09-649-866A-1102
20	48	33.1	140	5	US-09-758-471-2894
21	48	33.1	445	1	PCT-US01-08631-45047
22	47.5	32.8	96	5	US-09-764-905-15545
23	47	32.4	209	5	US-09-895-793-897
24	47	32.4	209	5	US-09-895-814-897
25	47	32.4	393	5	US-09-895-793-934
26	47	32.4	393	5	US-09-895-814-934
27	47	32.4	492	5	US-09-895-793-935

28	47	32.4	492	5	US-09-895-793-932	Sequence 932, App
29	47	32.4	492	5	US-09-895-814-895	Sequence 895, App
30	47	32.4	492	5	US-09-895-814-932	Sequence 932, App
31	47	32.4	492	5	US-09-806-428-6	Sequence 6, Appli
32	47	32.4	543	5	US-09-902-540-15614	Sequence 15614, A
33	47	32.4	701	1	PCT-US01-08631-31748	Sequence 31748, A
34	46.5	32.1	708	5	US-09-945-258-16	Sequence 16, Appl
35	46	31.7	91	5	US-09-760-443-836	Sequence 836, App
36	46	31.7	91	5	US-09-760-469-1777	Sequence 1777, Ap
37	46	31.7	91	5	US-09-760-476-1965	Sequence 1965, Ap
38	46	31.7	225	5	US-09-758-470-579	Sequence 579, App
39	46	31.7	231	5	US-09-758-470-408	Sequence 408, App
40	46	31.7	862	5	US-09-902-540-11888	Sequence 11888, A
41	45.5	31.4	100	5	US-09-764-905-12815	Sequence 12815, A
42	45.5	31.4	139	1	PCT-US01-08656-5757	Sequence 5757, Ap
43	45	31.0	122	5	US-09-758-472-6570	Sequence 6570, Ap
44	45	31.0	219	1	PCT-US01-14827-9756	Sequence 9756, Ap
45	45	31.0	355	5	US-09-803-110-13250	Sequence 13250, A

ALIGNMENTS

RESULT 1
US-09-922-378-2
; Sequence 2, Application US/099222378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-378-2

Query Match 100.0%; Score 145; DB 5; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26
|||||
Db 143 QSSSWTRVFQSWDRNLGRGSSAPSQ 168

RESULT 2
US-09-922-378-3
; Sequence 3, Application US/099222378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-922-378-3

Query Match 82.8%; Score 120; DB 5; Length 204;

```
0; Gaps 0;
```

OTHER INFORMATION: Xaa = X or * as defined in Table 2

; LOCATION: (20)..(75)


```
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (461)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-758-447-658

Query Match          34.5%; Score 50; DB 5; Length 1223;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 QSSS-----WTRVFSWDRN 16
||||| 1 11111111
Db 1083 QSSRRFVVVMKQVTSYDTN 1104

RESULT 11
US-09-764-905-10865
; Sequence 10865, Application US/09764905
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004
; CURRENT APPLICATION NUMBER: US/09/764,905
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
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OTHER INFORMATION: identified by eMATRIX, accession number BL00030B, p-value=9.526e-09, raw score of 7.03
NAME/KEY: DOMAIN
LOCATION: (185)...(350)
OTHER INFORMATION: RNA recognition motif. domain identified by Pfam, accession
NAME/KEY: misc.feature
LOCATION: (1)...(458)
OTHER INFORMATION: xaa = X or * as defined in Table 2
PCT-US01-14827-9450

Query Match 33.8%; Score 49; DB 1; Length 458;
Best Local Similarity 34.8%; Pred. No. 56;
Matches 8; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSA 23
| :||:| :||:| :||
Db 380 QGQWWTQGFNNYDQGYGNNSA 402

RESULT 14
PCT-US01-08656-8991
Sequence 8991, Application PC/TUS0108656
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
SEQ ID NO 8991
LENGTH: 1189
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (649)...(669)
OTHER INFORMATION: CORONAVIRUS NUCLEOCAPSID PROTEIN domain identified by
OTHER INFORMATION: eMATRIX, accession number DM01206B, p-value=4.646e-09, raw score
PCT-US01-08656-8991

Query Match 33.8%; Score 49; DB 1; Length 1189;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 SSWTRVFQSWDRNLGRG 20
:||:| :||:| :||
Db 780 NSWNKFGSGWNSNRGRG 797

RESULT 15
PCT-US01-08656-7468
Sequence 7468, Application PC/TUS0108656
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: PCT/US01/08656
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom

SEQ ID NO 7468
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(209)
OTHER INFORMATION: xaa = X or * as defined in Table 2
PCT-US01-08656-7468

Query Match 33.4%; Score 48.5; DB 1; Length 209;
Best Local Similarity 40.6%; Pred. No. 32;
Matches 13; Conservative 5; Mismatches 7; Indels 7; Gaps 2;

QY 2 SSWTRVFQS-----WWDRLGR-GSSAPSQ 26
| :||:| :||:| :||
Db 81 SSSFSRISFSVSGICPMWDSRDGEVGTTPSQ 112

Search completed: October 9, 2001, 16:08:32
Job time: 382 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:53:27 ; Search time 44.37 Seconds
(without alignments)
35.525 Million cell updates/sec

Title: US-09-580-523-1_COPY_143_168

Perfect score: 145

Sequence: 1 OSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
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20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	145	100.0	168	19	AAW55779 Human Bcl-xL/Bcl-2
2	145	100.0	168	21	AA13512 Human cell prolif
3	145	100.0	168	22	AA13512 Human cell prolif
4	145	100.0	168	22	AA13512 Human cell prolif
5	139	95.9	166	18	AA13512 Human cell prolif
6	120	82.8	162	22	AA13512 Human cell prolif
7	120	82.8	204	17	AA13512 Human cell prolif
8	120	82.8	204	19	AA13512 Human cell prolif
9	120	82.8	204	19	AA13512 Human cell prolif
10	120	82.8	204	19	AA13512 Human cell prolif
11	120	82.8	204	19	AA13512 Human cell prolif

12	120	82.8	204	19	AAW58832	Murine BAD protein
13	120	82.8	204	22	AAW70369	Longer murine BAD
14	84	57.9	16	17	AA13512	bcl-x(L)/bcl-2 ass
15	81	55.9	16	17	AA13512	bcl-x(L)/bcl-2 ass
16	51	35.2	247	22	AA13512	Human secreted pro
17	51	35.2	855	13	AA13512	Env polypeptide of
18	51	35.2	855	15	AA13512	FIV JAPAN2 envel
19	50	34.5	138	20	AA13512	Human testis speci
20	50	34.5	158	15	AA13512	FIV UK5 envelope p
21	50	34.5	1152	21	AA13512	Human thrombospond
22	50	34.5	1170	22	AA13512	Human variant thro
23	49	33.8	137	20	AA13512	Rat sperm coating
24	49	33.8	155	22	AA13512	Human prostate can
25	49	33.8	225	22	AA13512	Human prostate can
26	49	33.8	242	15	AA13512	FIV ITALYM4 envelo
27	49	33.8	646	22	AA13512	Human prostate can
28	49	33.8	1148	20	AA13512	Renal cancer assoc
29	48.5	33.4	350	21	AA13512	Streptomyces nogal
30	48	33.1	241	15	AA13512	FIV UK14 envelope
31	48	33.1	3054	14	AA13512	Translation of TEV
32	47	32.4	492	21	AA13512	Human TMPSR22 prot
33	47	32.4	492	21	AA13512	HrPCA6/7 polypepti
34	47	32.4	492	21	AA13512	Ovrl15 homolog pro
35	47	32.4	492	21	AA13512	Human tumour suppr
36	47	32.4	492	21	AA13512	Human 20p1F12-GTC2
37	46.5	32.1	695	22	AA13512	Mouse Dishevelled-
38	46.5	32.1	708	21	AA13512	Mouse PAMP protein
39	46	31.7	18	16	AA13512	Subpeptide 4N of t
40	46	31.7	30	16	AA13512	Thrombospondin 1 (
41	46	31.7	30	17	AA13512	Cell binding domai
42	46	31.7	111	21	AA13512	Human ORFX ORF1286
43	46	31.7	219	19	AA13512	Human LEA-motif de
44	46	31.7	240	15	AA13512	FIV DUTCH6 envelop
45	46	31.7	373	14	AA13512	Grass pollen aller

ALIGNMENTS

RESULT 1

AAW55779
ID AAW55779 standard; Protein: 168 AA.

XX AC AAW55779;

XX DT 17-JUL-1998 (first entry)

XX DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;

XX KW programmed cell death; apoptosis.

XX OS Homo sapiens.

XX PN WO9812328-A2.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-US16991.

XX PR 20-SEP-1996; 96US-0717123.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Horne WA, Oltersdorf T;

XX DR WPI; 1998-217267/19.

XX DR N-PSDB; AAV25877.

XX XX bcl-x(L)/bcl-2 ass

PT Murine BCL-XL/BCL-

PT Mutant BCL-XL/BCL-

PS Mutant BCL-XL/BCL-
used to develop products for treating
e.g. neurodegenerative disease, cancers or autoimmune disease
Claim 8; Fig 1; 4lpp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL
 CC results in the induction of programmed cell death, i.e. apoptosis.
 CC Bad can be used in screening assays for compounds to treat or
 CC prevent diseases characterised by apoptotic cell death, such as
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
 CC aplastic anaemia and ischaemic injury including myocardial
 CC infarction, stroke and reperfusion injury. Assays can also be
 CC used to obtain apoptosis enhancing compounds to treat or prevent
 CC diseases characterised by the loss of apoptotic cell death, such as
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated
 CC glomerulonephritis and viral infections, e.g. herpesvirus,
 CC poxvirus or adenovirus infection. Bad can also be used for
 CC detection and diagnosis.
 XX

XX Sequence 168 AA;
 SQ

Query Match 100.0%; Score 145; DB 19; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.le-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWMDRLGRGSSAPSQ 26
 Db 143 qssswtrvfqswmdrlgrgssapsq 168
 |||||

RESULT 2
 AAB13512
 ID AAB13512 standard; protein; 168 AA.
 XX
 AC AAB13512;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Human cell proliferation protein APOP-1.
 XX
 KW Human; cell proliferation; APOP-1; cancer; inflammation; infection;
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN US6080847-A.
 XX
 PD 27-JUN-2000.
 XX
 PF 04-DEC-1997; 97US-0985335.
 XX
 PR 04-DEC-1997; 97US-0985335.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Corley NC, Hillman JL, Yue H, Lal P, Shah P;
 XX
 DR WPI: 2000-451230/39.
 DR N-PSDB; AAB63332.
 XX
 PT Novel polynucleotide and polypeptide sequences of proteins associated
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.
 PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease -
 XX
 PS Example 8; Fig 1; 58pp; English.
 XX

The present sequence is the human APOP-1 protein. This protein, which
 CC shares structural and chemical homology with Bcl-2, is involved in cell
 CC proliferation. Its coding sequence was isolated by screening a synovial
 CC tissue cDNA library using a computer search for amino acid sequence
 CC alignments. The gene and protein can be used in the treatment of various
 CC cancers, disorders with associated inflammation such as Addison's

CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
 CC of cancer, haemodialysis and extracorporeal circulation, infections,
 CC trauma, disorders with associated apoptosis including AIDS and other
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
 CC such as myocardial infarction, and wasting diseases including cachexia.
 XX

XX Sequence 168 AA;
 SQ

Query Match 100.0%; Score 145; DB 21; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.le-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWMDRLGRGSSAPSQ 26
 Db 143 qssswtrvfqswmdrlgrgssapsq 168
 |||||

RESULT 3
 AAB70368
 ID AAB70368 standard; protein; 168 AA.
 XX
 AC AAB70368;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Human BAD mutant amino acid sequence SEQ ID NO:1.
 XX
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nontropic; antischismic; vulnerary;
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200110888-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 30-MAY-2000; 2000WO-US11864.
 XX
 PR 28-MAY-1999; 99US-0136783.
 XX
 PA (APOP-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX
 DR WPI: 2001-138734/14.
 XX
 PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Claim 1; Page 147; 157pp; English.
 XX

The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC nontropic, antischismic, vulnerary, cytostatic, antiviral,

CC antiarthritic, antiinflammatory and immunosuppressive activities, and
CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
CC polynucleotides can be used for screening candidate compounds and drugs
CC for activity that promote cell survival or apoptosis. Other uses include
CC inducing or inhibiting apoptosis in a cell. Candidate compounds
CC identified and (mutant) BAD polypeptides are useful in treating
CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
CC death, reperfusion cell death, wound healing, cancer, viral infections,
CC lymphoproliferative conditions, arthritis, infertility, inflammation and
CC autoimmune diseases. The present sequence represents a specifically
CC claimed human BAD mutant amino acid sequence from the present invention.
XX
SQ Sequence 168 AA;

Query Match 100.0%; Score 145; DB 22; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
|||||
DB 143 qsswtrvfqswdrnlgrgssapsq 168

RESULT 4
AAB48287
ID AAB48287 standard; protein; 168 AA.
XX
AC AAB48287;
DT 02-APR-2001 (first entry)
DE Human Bad protein.
KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytostatic.
OS Homo sapiens.
XX
PN WO200075184-A1.
PD 14-DEC-2000.
XX
PF 05-JUN-2000; 2000WO-US15449.
XX
PR 04-JUN-1999; 99US-0137494.
XX
PA (UYUA) UNIV YALE.
PI Zhang H, Tsvetkov LM, Kondo T;
XX WPI; 2001-061703/07.
DR N-PSDB; AAC84599.
XX

Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins -
XX
PS Claim 5; Page 102-103; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
CC cell, using proteins selected from S-phase kinase associated proteins 1
CC and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the
CC cullin/ CDC53 family of proteins). The method is useful for altering the
CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
CC that modulate interactions between SKP and target proteins are useful for
XX treating tumours.
XX
SQ Sequence 168 AA;

Query Match 100.0%; Score 145; DB 22; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
|||||
DB 143 qsswtrvfqswdrnlgrgssapsq 168

RESULT 5
AAW32476
ID AAW32476 standard; Protein; 166 AA.
XX
AC AAW32476;
DT 15-JAN-1998 (first entry)
DE BBC6 protein for regulating cell death.
XX
KW BBC6 gene; cell death; cell cycle; Bcl2; human.
XX
OS Homo sapiens.
XX
PN US5663316-A.
PD 02-SEP-1997.
XX
PF 18-JUN-1996; 96US-0665617.
XX
PR 18-JUN-1996; 96US-0665617.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Xudong Y;
XX
DR WPI; 1997-447980/41.
DR N-PSDB; AAT91561.
XX

PT Isolated BBC6 gene - encodes a protein that regulates cell death
PT through interaction with Bcl-2

PS Claim 1; Column 11-12; 7pp; English.

XX The present sequence represents a protein of 166 amino acids. The
CC sequence is disclosed as being a protein called BBC6 which regulates
CC cell death through interaction with Bcl-2. The DNA may be used for the
CC production of the recombinant protein, which can be used in unspecified
CC therapeutic or diagnostic procedures, as a molecular weight marker, and
CC to raise antibodies that can be used in unspecified diagnostic or
CC therapeutic applications and to reduce or eliminate the biological
CC activity of the BBC6 protein in vivo.
XX
SQ Sequence 166 AA;

Query Match 95.9%; Score 139; DB 18; Length 166;
Best Local Similarity 92.3%; Pred. No. 7.8e-13;
Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
|||||
DB 141 qsswtrvfqswdrnlgrgtaapsq 166

RESULT 6
AAB70370
ID AAB70370 standard; protein; 162 AA.
XX
AC AAB70370;
XX
DT 02-MAY-2001 (first entry)
XX

DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunosuppressant; neuroprotective; nootropic; antiischaemic; vulnerary;
 KW cytoskeletal; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.

XX Mus musculus.

OS Synthetic.

XX WO200110888-A1.

PD 15-FEB-2001.

XX 30-MAY-2000; 2000WO-US11864.

XX 28-MAY-1999; 99US-0136783.

XX (APOP-) APOPTOSIS TECHNOLOGY INC.

XX Zhou X;

XX WPI; 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -

PS Claim 7; Page 148-149; 157pp: English.

XX The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC nootropic, antiischaemic, vulnerary, cytoskeletal, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed shorter murine BAD mutant amino acid sequence from the present
 CC invention.

XX Sequence 162 AA;

Query Match 82.8%; Score 120; DB 22; Length 162;
 Best Local Similarity 73.1%; Pred. No. 4.5e-10;
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 137 qsagwtrlii qswdrnlgrgsgtspq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AAR95168;

XX 06-JAN-1997 (first entry)

XX bcl-x(L)/bcl-2 associated death promoter protein.

DE Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX Mus musculus.

XX Key Location/Qualifiers

FT Region 147..149

FT /note= "BH1 conserved amino acids"

FT Region 191..192

FT /note= "BH2 conserved amino acids"

FT Domain 38..61

FT /note= "PEST sequence"

FT Domain 111..130

FT /note= "PEST sequence"

XX WO9613614-A1.

XX 09-MAY-1996.

XX 31-OCT-1995; 95WO-US14246.

XX 31-OCT-1994; 94US-0333565.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1996-251465/25.

XX N-PSDB; AAT29479.

XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
 PT useful to treat neoplasia and apoptosis and to identify agents
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heterodimers
 PS Claim 3; Fig 1; 130pp: English.

XX This sequence represents the murine bcl-x(L)/bcl-2 associated death
 CC promoter (Bad) gene. Bad is a 22.1 kb protein which interacts with
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
 CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad
 CC has been found to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
 CC death inhibitory activity of bcl-x(L), but is much less effective at
 CC countering the death inhibitory activity of bcl-2. Bad expression can
 CC accelerate apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the
 CC death repressor activity of bcl-x(L). Bad competes with Bax for binding
 CC to bcl-x(L). Bad may be used to identify agents which inhibit its
 CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,
 CC e.g. AIDS, senescence or ischaemia.

XX Sequence 204 AA;

Query Match 82.8%; Score 120; DB 17; Length 204;
 Best Local Similarity 73.1%; Pred. No. 5.8e-10;
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 179 qsagwtrlii qswdrnlgrgsgtspq 204

RESULT 8

AAR61315

ID AAR61315 standard; Protein; 204 AA.

XX

AC AAW61315;
XX
DT 07-OCT-1998 (first entry)
XX
DE Murine BCL-XL/BCL-2 associated cell death regulator.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
XX
XX WO9817682-A1.
PN
PD 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
PF
XX 18-OCT-1996; 96US-0733505.
PR
XX (UNIW) UNIV WASHINGTON.
PA
XX Korsmeyer SJ;
PI
XX WPI; 1998-261422/23.
DR N-PSDB; AAV27833.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 1; Fig 10; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence is the murine BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 19; Length 204;
Best Local Similarity 73.1%; Pred. No. 5.8e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
||: |||: |||||: |||
Db 179 qsgwttriiqswdrnlkggstpsq 204

RESULT 9
AAW61316
ID AAW61316 standard; Protein; 204 AA.
XX
AC AAW61316;

XX 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
XX
XX WO9817682-A1.
PN
PD 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
PF
XX 18-OCT-1996; 96US-0733505.
PR
XX (UNIW) UNIV WASHINGTON.
PA
XX Korsmeyer SJ;
PI
XX WPI; 1998-261422/23.
DR N-PSDB; AAV27834.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 7; Page 59; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 19; Length 204;
Best Local Similarity 73.1%; Pred. No. 5.8e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26
||: |||: |||||: |||
Db 179 qsgwttriiqswdrnlkggstpsq 204

RESULT 10
AAW61317
ID AAW61317 standard; Protein; 204 AA.
XX
AC AAW61317;

```
XX 07-OCT-1998 (first entry)
DT
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX W09817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
XX
XX 18-OCT-1996; 96US-0733505.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
XX
XX N-PSDB; AAV27835.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX
XX Claim 7; Page 60; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischaemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
```

Query Match 82.8%; Score 120; DB 19; Length 204;
Best Local Similarity 73.1%; Pred. NO. 5.8e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26
||: |||: ||||| |||: |||
Db 179 qsagwtrilqswdrnlkggstpsq 204

RESULT 11
AAW61318
ID PAAW61318 standard; Protein; 204 AA.
XX AAW61318;
AC

```
XX 07-OCT-1998 (first entry)
DT
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX W09817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
XX
XX 18-OCT-1996; 96US-0733505.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
XX
XX N-PSDB; AAV27835.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX
XX Claim 7; Page 60-61; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischaemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;
```

Query Match 82.8%; Score 120; DB 19; Length 204;
Best Local Similarity 73.1%; Pred. NO. 5.8e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26
||: |||: ||||| |||: |||
Db 179 qsagwtrilqswdrnlkggstpsq 204

RESULT 12
AAW58832
ID AAW58832 standard; protein; 204 AA.
XX
AC AAW58832;

XX 23-JUL-1998 (first entry)
 XX Murine BAD protein.
 DE
 XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
 KW serine phosphorylation; post-translational modification; apoptosis;
 KW signal transduction regulator; phosphoserine phosphatase; senescence;
 KW immunodeficiency disease; neurodegenerative disease; infertility;
 KW cancer, viral infection; lymphoproliferative condition; arthritis;
 KW inflammation; autoimmune diseases.
 XX
 OS Mus sp.
 XX
 PN WO9809643-A1.
 XX
 PD 12-MAR-1998.
 XX
 XX 09-SEP-1997; 97WO-US15871.
 PF
 XX 09-SEP-1996; 96US-0707868.
 PR
 XX (UNITW) UNIV WASHINGTON.
 PA
 XX Korsmeyer SJ;
 PI
 XX WPI; 1998-207049/18.
 DR
 XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
 PT polypeptide - useful for modulation of apoptosis associated with,
 PT e.g. cancer and immunodeficiency diseases
 PT
 XX Claim 3; Fig 8; 61pp; English.
 PS
 XX This sequence represents a novel serine-phosphorylated protein, BAD
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
 CC phosphorylated in a post-translational modification and allows binding
 CC to the 14-3-3 protein which is a signal transduction regulator.
 CC Modulators of phosphorylated BAD, which act through inhibition/activation
 CC of a phosphoserine phosphatase, are useful for preventing/treating
 CC increased/decreased apoptosis in a cell. The increased apoptosis may
 CC result from immunodeficiency diseases, senescence, neurodegenerative
 CC disease, ischaemic cell death, reperfusion cell death, infertility and
 CC wound-healing. Decreased apoptosis may result from cancer, viral
 CC infection, lymphoproliferative conditions, arthritis, infertility,
 CC inflammation and autoimmune diseases. Measuring the amount of
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total
 CC BAD in a cell is useful for determining the apoptotic state of a cell.
 XX
 SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 19; Length 204;
 Best Local Similarity 73.1%; Pred. No. 5.8e-10;
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26
 ||: |||: ||||| |||: | |||
 Db 179 qsagwtrliqswdrnlqg9gstpsq 204

RESULT 13
 AAB70369
 ID AAB70369 standard; protein; 204 AA.
 XX
 AC AAB70369;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
 XX
 KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; neutrotropic; antiischaemic; vulnerary;

KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS Mus musculus.
 OS Synthetic.
 PN WO200110888-A1.
 XX
 PD 15-FEB-2001.
 XX
 XX 30-MAY-2000; 2000WO-US11864.
 PF
 XX 28-MAY-1999; 99US-0136783.
 PR
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 PA
 XX Zhou X;
 PI
 XX WPI; 2001-138734/14.
 DR
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 PT
 XX Claim 4; Page 148; 157pp; English.
 PS
 XX The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC antiarthritic, antiischaemic, vulnerary, cytostatic, antiviral,
 CC antitumor, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed longer murine BAD mutant amino acid sequence from the present
 CC invention.
 XX
 SQ Sequence 204 AA;

Query Match 82.8%; Score 120; DB 22; Length 204;
 Best Local Similarity 73.1%; Pred. No. 5.8e-10;
 Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26
 ||: |||: ||||| |||: | |||
 Db 179 qsagwtrliqswdrnlqg9gstpsq 204

RESULT 14
 AAR95167
 ID AAR95167 standard; peptide; 16 AA.
 XX
 AC AAR95167;
 XX
 DT 03-JAN-1997 (first entry)
 XX
 DE bcl-x(L)/bcl-2 associated death promoter epitope, residues 182-197.
 XX
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.

OS Mus musculus.

XX WO9613614-A1.

XX 09-MAY-1996.

XX 31-OCT-1995; 95WO-US14246.

XX 31-OCT-1994; 94US-0333565.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1996-251465/25.

XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
 PT useful to treat neoplasia and apoptosis and to identify agents
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

XX Claim 2; Page 103; 130pp; English.

XX The sequences given in AAR95155-67 represent epitopes derived from the
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-
 CC related family clustered in the BH1 and BH2 domain. Bad has been found
 CC to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in
 CC vivo in mammalian cells. Overexpressed Bad counters the death
 CC inhibitory activity of bcl-x(L), but is much less effective at countering
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
 CC cell line expressing bcl-x(L), and its also counters the death repressor
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).
 CC Bad may be used to identify agents which inhibit its binding to bcl-2
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
 CC senescence or ischaemia.

XX Sequence 16 AA;

Query Match 57.9%; Score 84; DB 17; Length 16;
 Best Local Similarity 80.0%; Pred. No. 6.1e-06;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 WTRVFQSWDRNLGR 19

Db |||: |||||
 2 wtrlgswdrnlgr 16

RESULT 15

ID AAR95165

AC AAR95165 standard; peptide; 16 AA.

XX AAR95165;

XX 03-JAN-1997 (first entry)

XX bcl-x(L)/bcl-2 associated death promoter epitope, residues 180-195.

DE Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;
 KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX Mus musculus.

XX WO9613614-A1.

XX 09-MAY-1996.

XX 31-OCT-1995; 95WO-US14246.

XX 31-OCT-1994; 94US-0333565.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1996-251465/25.

XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
 PT useful to treat neoplasia and apoptosis and to identify agents
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

XX Claim 2; Page 103; 130pp; English.

XX The sequences given in AAR95155-67 represent epitopes derived from the
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-
 CC related family clustered in the BH1 and BH2 domain. Bad has been found
 CC to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in
 CC vivo in mammalian cells. Overexpressed Bad counters the death
 CC inhibitory activity of bcl-x(L), but is much less effective at countering
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
 CC cell line expressing bcl-x(L), and its also counters the death repressor
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).
 CC Bad may be used to identify agents which inhibit its binding to bcl-2
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
 CC senescence or ischaemia.

XX Sequence 16 AA;

Query Match 55.9%; Score 81; DB 17; Length 16;
 Best Local Similarity 75.0%; Pred. No. 1.7e-05;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNL 17

Db ||: |||: |||||
 1 sagwtrlgswdrnl 16

Search completed: October 9, 2001, 15:53:28
 Job time: 204 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:55:21 ; Search time 17.79 seconds

(without alignments)
50.064 Million cell updates/sec

Title: US-09-580-523-1_COPY_143_168

Perfect score: 145

Sequence: 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	145	100.0	168	BAD_HUMAN	Q92934 homo sapien
2	120	82.8	204	BAD_MOUSE	Q61337 mus musculus
3	65	44.8	419	NOEE_RHISN	P55472 rhizobium s
4	57	39.3	245	CRS3_HUMAN	P54108 homo sapien
5	57	39.3	3068	POLG_PEMVC	Q01500 p genome po
6	54	37.2	1632	CTPI_MYCTU	G10900 mycobacteri
7	54	37.2	3164	POLG_TUNVJ	P89509 t genome po
8	53	36.6	3163	POLG_TUNVQ	Q02597 t genome po
9	51	35.2	855	ENV_FIVT2	Q02282 feline immu
10	50	34.5	243	TPX1_HUMAN	P16562 homo sapien
11	50	34.5	1170	TSPI_BOVIN	Q28178 bos taurus
12	50	34.5	1170	TSPI_HUMAN	P07996 homo sapien
13	50	34.5	1170	TSPI_MOUSE	P35441 mus musculus
14	50	34.5	3061	POLG_PVTHU	Q02963 p genome po
15	50	34.5	3063	POLG_PVYN	P18247 p genome po
16	49.5	34.1	335	MAUG_METME	Q50233 methylophil
17	49.5	34.1	361	VAL1_TMOV	Q06657 tomato mott
18	49	33.8	246	AEQ_RAT	P12020 rattus norv
19	48	33.1	3054	POLG_TEV	P04517 t genome po
20	48	33.1	3066	POLG_BCMVN	Q65399 b genome po
21	48	33.1	3255	POLG_LMYO	P31999 l genome po
22	48	33.1	3255	POLG_LMYE	P89876 l genome po
23	47.5	32.8	3082	POLG_ZYMVS	Q36979 z genome po
24	47	32.4	462	MPPB_YEAST	P10507 saccharomyc
25	47	32.4	432	TMS2_HUMAN	Q15393 homo sapien
26	47	32.4	1926	LPH_RABIT	P09849 oryctolagus
27	46.5	32.1	695	DVLI_MOUSE	P51141 mus musculus
28	46.5	32.1	695	DVLI_RAT	Q9WB99 rattus norv
29	46.5	32.1	708	NICA_MOUSE	P57716 mus musculus
30	46	31.7	244	TPX1_CAVPO	Q60477 cavia porce
31	46	31.7	260	MTM2_MORBO	P23192 moraxella b
32	46	31.7	314	YMA3_BACST	Q45633 bacillus st
33	46	31.7	373	MP91_POAPR	P22284 poa pratens

34	46	31.7	441	1	SECY_MYCTU	P94926 mycobacteri
35	46	31.7	854	1	ENV_FIVWO	Q05312 feline immu
36	45.5	31.4	431	1	PHOR_ECOLI	P08400 escherichia
37	45.5	31.4	431	1	PHOR_KLEPN	P45608 klebsiella
38	45.5	31.4	431	1	PHOR_SHIDY	P45609 shigella dy
39	45.5	31.4	518	1	VG47_HSV11	Q00139 ictaluriid h
40	45.5	31.4	3083	1	POLG_ZYMYR	Q89330 z genome po
41	45	31.0	353	1	VAL1_BGMV	P05175 bean golden
42	45	31.0	394	1	PEPA_ASPAW	P17946 aspergillus
43	45	31.0	856	1	ENV_FIVPE	P16090 feline immu
44	45	31.0	1146	1	MMLC_MYCTU	Q50585 mycobacteri
45	44.5	30.7	953	1	YM8G_YEAST	Q03516 saccharomyc

ALIGNMENTS

RESULT 1	BAD_HUMAN	STANDARD;	PRT;	168 AA.
ID	BAD_HUMAN			
AC	Q92934;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	BAD PROTEIN (BCL-2 BINDING COMPONENT 6).			
GN	BAD OR BIC6 OR BCL2L8.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE			
CC	BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL			
CC	HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE			
CC	THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2			
CC	(BY SIMILARITY).			
CC	-!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH			
CC	BAX, MCL-1, A1, OR BCL-X(S) (BY SIMILARITY).			
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.			
CC	-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).			
CC	-!- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).			
CC	-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
EMBL;	U66879; AAB36516.1; -			
DR	MIM; 603167; -			
KW	Apoptosis.			
FT	DOMAIN 101 121 BH1.			
FT	DOMAIN 146 163 BH2.			
SQ	SEQUENCE 168 AA; 18408 MW; BDF3D99587C222BE CRC64;			

Query Match 100.0%; Score 145; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 7.7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26

Db 143 QSSSWTRVFQSWDRNLGRGSSAPSQ 168

RESULT 2

BAD_MOUSE

ID BAD_MOUSE STANDARD; PRT; 204 AA.
AC Q61337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
GN BAD OR BBC6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain, and Thymus;
RC MEDLINE=951136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boile L.H., Thompson C.B., Korsmeyer S.J.;
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and promotes cell death.";
RL Cell 80:285-291(1995).
CC -!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
CC -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH BAX, MCL-1, AL, OR BCL-X(S).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; L37296; AAA64465.1; -;
DR MGD; MGI:1096330; Bad.
KW Apoptosis.
FT DOMAIN 138 158 BH1.
FT DOMAIN 182 199 BH2.
FT SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;
SQ
Query Match 82.8%; Score 120; DB 1; Length 204;
Best Local Similarity 73.1%; Pred. No. 3.3e-10;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 QSSSWTRVFQSWDRNLGRGSSAPSQ 26
II: |||: |||||: |||: |||
DB 179 QSAGWTRIIQSWDRNLGRGSGTPSQ 204
RESULT 3
NOEE_RHISN STANDARD; PRT; 419 AA.
AC P55472; P72326;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NODULATION PROTEIN NOEE (EC 2.8.2.-).
GN NOEE OR Y4HB.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97361801; PubMed=9218762;
RA Hanlin M., Jabbouri S., Quesada-Vincens S., Freiberg C., Perret X., Broughton W.J., Fellay R.;
RT "Sulphation of Rhizobium sp. NGR234 nod factors is dependent on noe, a new host-specificity gene.";
RN Mol. Microbiol. 24:1119-1129(1997).
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A., Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
CC -!- FUNCTION: REQUIRED FOR THE FORMATION OF SULFATED NOD FACTOR. PROPOSED TO TRANSFER ACTIVATED SULFATE (PAPS) TO THE FUCOSE OF THE NOD FACTOR.
CC -!- SIMILARITY: LIMITED TO NODH AND TO C.ELEGANS F42G9.8.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; Y09415; CAA70569.1; -;
DR EMBL; AE000076; AAB91690.1; -;
KW Nodulation; Transferrase; Plasmid.
SQ SEQUENCE 419 AA; 46569 MW; 848C48E0416AAALF CRC64;
Query Match 44.8%; Score 65; DB 1; Length 419;
Best Local Similarity 47.6%; Pred. No. 0.044;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 5 WTRVFQSWDRNLGRGSSAPS 25
II: |||||: |||: |||:
DB 308 YRRVFTWMDLRGEGEGIPA 328
RESULT 4
CRS3_HUMAN STANDARD; PRT; 245 AA.
ID CRS3_HUMAN
AC P54108; Q15512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYSTEINE-RICH SECRETORY PROTEIN-3 PRECURSOR (CRISP-3) (SGP28 PROTEIN).
GN CRISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270732; PubMed=8665901;
RA Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D., Donner P., Schleuning W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96186934; PubMed=8601434;
RA Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
RT "SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with similarity to a human testis-specific gene product and a rodent sperm-coating glycoprotein.";
RL FEBS Lett. 380:246-250(1996).
CC -!- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN SPECIFIC GRANULES.
CC -!- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE > EPIDIDYMIS, OVARY, THYMUS AND COLON.
CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

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CC EMBL; X95240; CAA64527.1; -
CC EMBL; X94323; CAA63984.1; -
CC HSSP; P04284; ICFE.
CC InterPro; IPR001283; -
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPXLIKE.
CC PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
CC Glycoprotein; Signal; Multigene family.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 245
CC CARBOHYD 239 239 N-LINKED (GLCNAC...) (POTENTIAL).
CC CONFLICT 106 106 S -> P (IN REF. 2).
CC SEQUENCE 245 AA; 27630 MW; B4DD79CB7AE9E5F9 CRC64;

Query Match 39.3%; Score 57; DB 1; Length 245;
Best Local Similarity 39.3%; Pred. No. 0.35;
Matches 11; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

Qy 2 SSSWTRVFQSWWDR-----NLGRGSSAPS 25
||||: |||:| :| | |

Db 106 SSSWSQAISQSWFDEYNDFGVGPKTPN 133
||||: |||:| :| | |

RESULT 5

ID POLG_PEMVC STANDARD; PRT; 3068 AA.
AC Q01500;
DT 01-OCT-1993 (Rel. 27, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA) (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48); COAT PROTEIN (CP)].
OS Pepper mottle virus (California isolate) (PeMV) (PepMov C).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=31737;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93033110; PubMed=14113501;
RX Vance V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.;
RT "The complete nucleotide sequence of pepper mottle virus genomic RNA: comparison of the encoded polyprotein with those of other sequenced potyviruses";
RT Virology 191:19-30(1992).
RL -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -1- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.

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CC EMBL; M96425; AAA46903.1; -
CC PIR; A44062; A44062.
CC MEROPS; C04.001; -
CC MEROPS; C06.001; -
CC MEROPS; S30.001; -

CC InterPro; IPR001205; -
CC InterPro; IPR001410; -
CC InterPro; IPR001456; -
CC InterPro; IPR001592; -
CC InterPro; IPR001650; -
CC InterPro; IPR001730; -
CC InterPro; IPR002540; -
CC Pfam; PF00270; DEAD_1.
CC Pfam; PF00863; Peptidase_C4; 1.
CC Pfam; PF00851; Peptidase_C6; 1.
CC Pfam; PF01577; Poty_P1; 1.
CC Pfam; PF00767; Poty_Coat; 1.
CC Pfam; PF00680; RNA_dep_RNA_pol; 1.
CC Pfam; PF00271; helicase_C; 1.
CC PRINTS; PR00966; NIAPOTYPTASE.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.

FT CHAIN 1 287 N-TERMINAL PROTEIN.
FT CHAIN 288 743 HELPER COMPONENT PROTEINASE.
FT CHAIN 744 ? PROTEIN P3.
FT CHAIN ? 1156 6 KDA PROTEIN 1.
FT CHAIN 1157 1790 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1791 1842 6 KDA PROTEIN 2.
FT CHAIN 1843 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2276 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2277 2795 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2796 3068 COAT PROTEIN.
FT BINDING 1906 COVALENT LINKAGE OF VIRAL RNA (BY SIMILARITY).
FT NP_BIND 1241 1248 ATP (POTENTIAL).
SQ SEQUENCE 3068 AA; 348651 MW; FD3458B837FDA7C2 CRC64;

Query Match 39.3%; Score 57; DB 1; Length 3068;
Best Local Similarity 50.0%; Pred. No. 4.4;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 9 FQSWWDRNLGRGSSAP 24
|:||||:| | | |

Db 1191 FESWWDQVARGFTIP 1206
|:||||:| | | |

RESULT 6

ID CTPI_MYCTU STANDARD; PRT; 1632 AA.
AC Q10900;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROBABLE CATION-TRANSPORTING ATPASE I (EC 3.6.1.-).
GN CTPI OR RV0107C OR MTCY251.26C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 CC -|- CATALYTIC ACTIVITY: ATP + H(2O) = ADP + ORTHOPHOSPHATE.
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). STRONGEST SIMILARITY TO EUKARYOTIC CALCIUM-
 CC ATPASE TRANSPORT SYSTEMS.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; 274410; CAA98940.1; -;
 DR Tuberculist; RV0107C; -;
 DR InterPro: IPR001757; -;
 DR InterPro: IPR001899; -;
 DR Pfam; PF00122; E1-E2_ATPase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00120; HATPASE.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT TRANSMEM 30 50 POTENTIAL.
 FT TRANSMEM 148 168 POTENTIAL.
 FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 315 335 POTENTIAL.
 FT TRANSMEM 358 378 POTENTIAL.
 FT TRANSMEM 637 657 POTENTIAL.
 FT TRANSMEM 673 693 POTENTIAL.
 FT TRANSMEM 778 798 POTENTIAL.
 FT TRANSMEM 921 941 POTENTIAL.
 FT TRANSMEM 969 989 POTENTIAL.
 FT TRANSMEM 997 1017 POTENTIAL.
 FT TRANSMEM 1401 1421 POTENTIAL.
 FT TRANSMEM 1432 1452 POTENTIAL.
 FT TRANSMEM 1547 1567 POTENTIAL.
 FT MOD_RES 1053 1053 PHOSPHORYLATION (BY SIMILARITY).
 FT SEQUENCE 1632 AA; 169606 MW; A29F651A55EF7F8 CRC64;

Query Match 37.2%; Score 54; DB 1; Length 1632;
 Best Local Similarity 71.4%; Pred. No. 6.2;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 WDRNLGRGSSAPSQ 26

Db 1576 WDRSPGRASSAPRQ 1589

RESULT 7

POLG_TUMVJ STANDARD; PRT; 3164 AA.

AC P89509;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER

DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN

DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);

DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
 DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
 DE COAT PROTEIN (CP)];
 DE COAT PROTEIN (CP)];
 OS Turnip mosaic virus (strain Japanese) (TUMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OX NCBI_TaxID=12230;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97079098; PubMed=8920830;
 RA Ohshima K., Tanaka M., Sako N.;
 RT "The complete nucleotide sequence of turnip mosaic virus RNA Japanese
 RT strain.";
 RL Arch. Virol. 141:1991-1997(1996).
 CC -|- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
 CC MAY BE INVOLVED IN REPLICATION.
 CC -|- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
 CC -|- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
 CC -|- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
 CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
 CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
 CC INDIVIDUAL PROTEINS.
 CC -|- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -|- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -|- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; D83184; BAA11836.1; -;
 DR InterPro: IPR001205; -;
 DR InterPro: IPR001410; -;
 DR InterPro: IPR001456; -;
 DR InterPro: IPR001592; -;
 DR InterPro: IPR001650; -;
 DR InterPro: IPR001730; -;
 DR InterPro: IPR002540; -;
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00863; Peptidase_C4; 1.
 DR Pfam; PF00851; Peptidase_C6; 1.
 DR Pfam; PF01577; Poly_P1; 1.
 DR Pfam; PF00767; Poly_coat; 1.
 DR Pfam; PF00880; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00271; helicase_C; 1.
 DR PRINTS; PR00966; NIAPOTYPASE.
 DR Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 362 N-TERMINAL PROTEIN.
 FT CHAIN 363 820 HELPER COMPONENT PROTEINASE.
 FT CHAIN 821 1175 PROTEIN P3.
 FT CHAIN 1176 1227 6 KDA PROTEIN 1.
 FT CHAIN 1228 1871 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1872 1924 6 KDA PROTEIN 2.
 FT CHAIN 1925 2116 GENOME-LINKED PROTEIN.
 FT CHAIN 2117 2359 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2360 2876 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 2877 3164 COAT PROTEIN.
 FT BINDING 1987 1987 COVALENT LINKAGE OF VIRAL RNA (BY
 FT SIMILARITY).
 FT NP_BIND 1313 1320 ATP (POTENTIAL).
 FT SEQUENCE 3164 AA; 357731 MW; 0DFC735CB3A5231F CRC64;

Query Match 37.2%; Score 54; DB 1; Length 3164;
 Best Local Similarity 44.4%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy 7 RVFOSWMDRNLGRGSSAP 24
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Db 1261 KTFASWNNHQLSRGFTIP 1278

RESULT 8
POLG_TUMVQ
ID POLG_TUMVQ STANDARD; PRT; 3163 AA.
AC Q02597;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (C1); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Turnip mosaic virus (strain Quebec) (TUMV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus
OX NCBI_TaxID=36396;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93057350; PubMed=1431807;
RA Nicolas O., Laliberte J.F.;
RT "The complete nucleotide sequence of turnip mosaic potyvirus RNA.";
RL J. Gen. Virol. 73:2785-2793(1992).
RN [2]
RN SEQUENCE OF 1534-3163 FROM N.A., AND PARTIAL SEQUENCE.
RP TREMBLAY M.F., NICOLAS O., SINHA R., LAZURE C., LALIBERTE J.F.;
RA "Sequence of the 3'-terminal region of turnip mosaic virus RNA and
RT the capsid protein gene.";
RL J. Gen. Virol. 71:2769-2772(1990).
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- PPM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PPM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
```


CC -1- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
 CC

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 CC -----

DR EMBL; AB005287; BAA21115.1; -;
 DR EMBL; X87618; CAA60950.1; -;
 DR EMBL; X87619; CAA60951.1; -;
 DR HSSP; P35555; 1EMO.
 DR GlycoSuiteDB; Q28178; -;
 DR InterPro; IPR000561; -;
 DR InterPro; IPR000884; -;
 DR InterPro; IPR001007; -;
 DR InterPro; IPR001881; -;
 DR Pfam; PF00008; EGF; 2;
 DR Pfam; PF00090; tsp_1; 3;
 DR Pfam; PF00093; wvc; 1;
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; -;
 DR PROSITE; PS01208; WMFC; 1;
 DR PROSITE; PS00092; TSP1; 3;
 DR Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 1170
 FT DOMAIN 19 232
 FT DOMAIN 19 232
 FT DOMAIN 316 373
 FT DOMAIN 379 430
 FT DOMAIN 435 491
 FT DOMAIN 492 548
 FT DOMAIN 549 587
 FT DOMAIN 588 645
 FT DOMAIN 646 690
 FT DOMAIN 723 758
 FT DOMAIN 759 781
 FT DOMAIN 782 817
 FT DOMAIN 818 840
 FT DOMAIN 841 878
 FT DOMAIN 879 914
 FT DOMAIN 915 950
 FT DOMAIN 951 1170

FT SITE 926 928
 FT DISULFID 270 270
 FT DISULFID 274 274
 FT DISULFID 551 562
 FT DISULFID 556 572
 FT DISULFID 575 586
 FT DISULFID 592 608
 FT DISULFID 599 617
 FT DISULFID 620 644
 FT DISULFID 650 663
 FT DISULFID 657 676
 FT DISULFID 678 689
 FT CARBOHYD 248 248
 FT CARBOHYD 360 360
 FT CARBOHYD 708 708
 FT CARBOHYD 1067 1067
 FT CARBOHYD 1085 1085
 FT CONFLICT 805 805
 SQ SEQUENCE 1170 AA; 129533 MW; 0DD6ADF3E5FA031A CRC64;
 BY SIMILARITY.
 THROMBOSPONDIN 1.
 HEPARIN-BINDING (POTENTIAL).
 WMFC.
 TSP TYPE-1 1.
 TSP TYPE-1 2.
 TSP TYPE-1 3.
 EGF-LIKE 1.
 EGF-LIKE 2.
 EGF-LIKE 3.
 EGF-LIKE 4.
 TSP TYPE-3 1.
 TSP TYPE-3 2.
 TSP TYPE-3 3.
 TSP TYPE-3 4.
 TSP TYPE-3 5.
 TSP TYPE-3 6.
 TSP TYPE-3 7.
 C-TERMINAL.
 CELL ATTACHMENT SITE (POTENTIAL).
 INTERCHAIN (PROBABLE).
 INTERCHAIN (PROBABLE).
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 S -> G (IN REF. 2).
 MW; 0DD6ADF3E5FA031A CRC64;

Query Match 34.5%; Score 50; DB 1; Length 1170;
 Best Local Similarity 50.08; Pred. No. 16;
 Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 1 QSSS-----WTRVFQSWDRN 16

Db 1030 QSSSRFVVMKQVTSYWDN 1051
 RESULT 12
 TSP1_HUMAN
 ID TSPI_HUMAN STANDARD; PRT; 1170 AA.
 AC P07996;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE THROMBOSPONDIN 1 PRECURSOR.
 GN THBS1 OR TSPI OR TSP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Endothelial cells;
 RX MEDLINE=87057617; PubMed=2430973;
 RA Lawler J., Hynes R.O.;
 RT "The structure of human thrombospondin, an adhesive glycoprotein with
 RT multiple calcium-binding sites and homologies with several different
 RT proteins.";
 RL J. Cell Biol. 103:1635-1648(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89139590; PubMed=2918029;
 RA Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,
 RA Baumgartel D.M., Rotwein P., Frazier W.A.;
 RT "Complete thrombospondin mRNA sequence includes potential regulatory
 RT sites in the 3' untranslated region.";
 RL J. Cell Biol. 108:729-736(1989).
 RN [3]
 RP SEQUENCE OF 1-397 FROM N.A.
 RX MEDLINE=87157592; PubMed=3030396;
 RA Kobayashi S., Eden-McCutchan F., Framson P., Bornstein P.;
 RT "Partial amino acid sequence of human thrombospondin as determined by
 RT analysis of cDNA clones: homology to malarial circumsporozoite
 RT proteins.";
 RL Biochemistry 25:8418-8425(1986).
 RN [4]
 RP SEQUENCE OF 1-374 FROM N.A.
 RX MEDLINE=86287276; PubMed=3461443;
 RA Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;
 RT "Characterization of a cDNA encoding the heparin and collagen binding
 RT domains of human thrombospondin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).
 RN [5]
 RP SEQUENCE OF 1-166 FROM N.A.
 RX MEDLINE=89291870; PubMed=2544587;
 RA Laherty C.D., Gierman T.M., Dixit V.M.;
 RT "Characterization of the promoter region of the human thrombospondin
 RT gene. DNA sequences within the first intron increase transcription.";
 RL J. Biol. Chem. 264:11222-11227(1989).
 RN [6]
 RP SEQUENCE OF 1028-1170 FROM N.A.
 RA Fleury M., Jobin C., Gauthier J., Kreis C.G.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
 CC CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
 CC LAMININ AND TYPE V COLLAGEN.
 CC -1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WMFC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
 CC -----
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DR EMBL; M62465; AAA50611.1; JOINED.
DR EMBL; M62466; AAA50611.1; JOINED.
DR EMBL; M62467; AAA50611.1; JOINED.
DR EMBL; M62468; AAA50611.1; JOINED.
DR EMBL; M62469; AAA50611.1; JOINED.
DR EMBL; M82276; AAA50611.1; JOINED.
DR EMBL; J05606; AAA40431.1; JOINED.
DR EMBL; J05605; AAA40431.1; JOINED.
DR PIR; A40558; A40558.
DR PIR; B42587; B42587.
DR PIR; A37905; A37905.
DR HSP; P35555; LEMO.
DR MGD; MGI:98737; Ths1.
DR InterPro; IPR000561; -.
DR InterPro; IPR000884; -.
DR InterPro; IPR001007; -.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00090; tsp_1; 3.
DR Pfam; PF00093; vwc; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00092; TSP1; 3.
DR PROSITE; PS01208; VWFC; 1.
DR Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
EGF-like domain; Signal.
FT SIGNAL 1 18
FT CHAIN 19 1170
FT DOMAIN 19 232
FT DOMAIN 316 373
FT DOMAIN 379 430
FT DOMAIN 435 491
FT DOMAIN 492 548
FT DOMAIN 549 587
FT DOMAIN 588 645
FT DOMAIN 646 690
FT DOMAIN 723 758
FT DOMAIN 759 781
FT DOMAIN 782 817
FT DOMAIN 818 840
FT DOMAIN 841 878
FT DOMAIN 879 914
FT DOMAIN 915 950
FT DOMAIN 951 1170
FT SITE 926 928
FT DISULFID 270 270
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FT DISULFID 551 562
FT DISULFID 556 572
FT DISULFID 575 586
FT DISULFID 592 608
FT DISULFID 599 617
FT DISULFID 620 644
FT DISULFID 650 663
FT DISULFID 657 676
FT DISULFID 678 689
FT CARBOHYD 248 248
FT CARBOHYD 360 360
FT CARBOHYD 708 708
FT CARBOHYD 1067 1067
FT CONFLICT 1025 1025
SQ SEQUENCE 1170 AA; 129646 MW; 0443E493615E7F06 CRC64;

Query Match 34.58; Score 50; DB 1; Length 1170;
Best Local Similarity 50.08; Pred. No. 16;
Matches 11; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy 1 QSSS-----WTRVFQSWDRN 16
||||| 1 1111111
Db 1030 QSSRFYVWMKQYTSWDRN 1051

RESULT 14

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POLG_PVYHU STANDARD; PRT; 3061 AA.
ID AC Q02963;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Potato virus Y (strain Hungarian) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Polyvirus.
OX NCBI_TaxID=31739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93154578; PubMed=8428653;
RA Thole V., Dalmay T., Burgyn J., Balazs E.;
RT "Cloning and sequencing of potato virus Y (Hungarian isolate) genomic
RT RNA.";
RL Gene 123:149-156(1993).
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M95491; AAB59762.1; -.
CC PIR; JN0545; JN0545.
CC MEROPS; C04.001; -.
CC MEROPS; C06.001; -.
CC MEROPS; S30.001; -.
CC InterPro; IPR001205; -.
CC InterPro; IPR001410; -.
CC InterPro; IPR001456; -.
CC InterPro; IPR001592; -.
CC InterPro; IPR001650; -.
CC InterPro; IPR001730; -.
CC InterPro; IPR002540; -.
CC Pfam; PF00270; DEAD; 1.
CC Pfam; PF00863; Peptidase_C4; 1.
CC Pfam; PF00851; Peptidase_C6; 1.
CC Pfam; PF01577; Poty_P1; 1.
CC Pfam; PF00767; Poty_coat; 1.
CC Pfam; PF00680; RNA_dep_RNA_pol; 1.
CC Pfam; PF00271; helicase_C; 1.
CC PRINTS; PR00366; NIAPOTYPTASE.
CC Hydrolyase; Transferase; Thiol protease; RNA-directed RNA polymerase;
CC Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
CC ATP-binding.
FT CHAIN 1 275 N-TERMINAL PROTEIN.
FT CHAIN 276 824 HELPER COMPONENT PROTEINASE.
FT CHAIN 825 ? PROTEIN P3.
FT CHAIN ? 1157 6 KDA PROTEIN 1.

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FT CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1792 1843 6 KDA PROTEIN 2.
FT CHAIN 1844 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2276 2794 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2795 3061 COAT PROTEIN.
FT BINDING 1907 1907 COAT PROTEIN.
FT NP_BIND 1242 1249 SIMILARITY.
FT SEQUENCE 3061 AA; 347326 MW; 737FFBA215B56F99 CRC64;
ATP (POTENTIAL).
Query Match 34.5%; Score 50; DB 1; Length 3061;
Best Local Similarity 43.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 9 FQSWDRNLGRGSSAP 24
| | | | | : : : : :
Db 1192 FSDWDRQIQMGHTLP 1207
| | | | | : : : : :
RESULT 15
POLG_PVYN STANDARD; PRT: 3063 AA
AC P18247; Q85266; Q85267; Q85268; Q85269; Q85270; Q85271; Q85272;
AC Q85273;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER
DE COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
DE 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KDA PROTEIN 2 (6K2);
DE GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NIA)
DE (EC 3.4.22.-) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
DE PROTEIN B (NI-B) (NIB) (RNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
DE COAT PROTEIN (CP)].
OS Potato virus Y (strain N) (PVY).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
OC Potyvirus.
OX NCBI_TaxID=12219;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89279275; PubMed=2732709;
RA Robaglia C., Durand-Tardif M., Tronchet M., Boudazin G.,
RA Astier-Manificier S., Casse-Delbart F.;
RT "Nucleotide sequence of potato virus Y (N Strain) genomic RNA.";
RL J. Gen. Virol. 70:935-947(1989).
RN [2]
RP REVISIONS.
RA Durand-Tardif M.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -!- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -!- PTM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -!- PTM: THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPROTEIN WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -!- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----

DR EMBL; X12456; CAA30988.1; -;
DR EMBL; D00441; BAA00342.1; -;
DR PIR; JS0166; JS0166.
DR MEROPS; C04.001; -;
DR MEROPS; C06.001; -;
DR MEROPS; S30.001; -;
DR InterPro; IPR001205; -;
DR InterPro; IPR001410; -;
DR InterPro; IPR001456; -;
DR InterPro; IPR001592; -;
DR InterPro; IPR001650; -;
DR InterPro; IPR001730; -;
DR InterPro; IPR002540; -;
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00863; Peptidase_C4; 1.
DR Pfam; PF00851; Peptidase_C6; 1.
DR Pfam; PF01577; Poty_P1; 1.
DR Pfam; PF00767; Poty_coat; 1.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00271; helicase_C; 1.
DR PRINTS; PR00966; NIAPOTYPTASE.
KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
KW ATP-binding.
FT CHAIN 1 275 N-TERMINAL PROTEIN.
FT CHAIN 276 824 HELPER COMPONENT-PROTEINASE.
FT CHAIN 825 ? PROTEIN P3.
FT CHAIN ? 1157 6 KDA PROTEIN 1.
FT CHAIN 1158 1791 CYTOPLASMIC INCLUSION PROTEIN.
FT CHAIN 1792 1843 6 KDA PROTEIN 2.
FT CHAIN 1844 ? GENOME-LINKED PROTEIN.
FT CHAIN ? 2275 NUCLEAR INCLUSION PROTEIN A.
FT CHAIN 2276 2796 NUCLEAR INCLUSION PROTEIN B.
FT CHAIN 2797 3063 COAT PROTEIN.
FT BINDING 1907 1907 COVALENT LINKAGE OF VIRAL RNA (BY
FT NP_BIND 1242 1249 SIMILARITY).
FT SEQUENCE 3063 AA; 347535 MW; 3EC79125DE33F1BB CRC64;
Query Match 34.5%; Score 50; DB 1; Length 3063;
Best Local Similarity 43.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 9 FQSWDRNLGRGSSAP 24
| | | | | : : : : :
Db 1192 FSDWDRQIQMGHTLP 1207
| | | | | : : : : :
Search completed: October 9, 2001, 15:55:22
Job time: 197 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:50:10 ; Search time 28.81 seconds
(without alignments)
444.197 Million cell updates/sec

Title: US-09-580-523-1
Perfect score: 905
Sequence: 1 MFQIPFEPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR68: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	71.7	204	2 A55671	bad protein - mous
2	95	10.5	834	2 T42702	hypothetical prote
3	93.5	10.3	1729	2 T18396	erythrocyte membra
4	93	10.3	1300	2 T03166	probable immediate
5	92.5	10.2	336	2 T30757	hypothetical prote
6	91.5	10.1	2248	2 A35938	profilaggrin - hum
7	90	9.9	646	1 S15901	chromogranin B pre
8	90	9.9	2237	2 T45115	N-type calcium cha
9	90	9.9	2339	2 A42566	omega-conotoxin-se
10	89.5	9.9	449	1 A41520	chromogranin A pre
11	88.5	9.8	393	2 JC5614	RNB6 protein - rat
12	86.5	9.6	1077	2 A44067	serine-rich protei
13	86.5	9.6	1647	2 S45252	SNF2beta protein -
14	86.5	9.6	2715	2 T13049	eyelid - fruit fly
15	86	9.5	222	2 T43500	hypothetical prote
16	86	9.5	270	1 WJMS13	homeotic protein H
17	86	9.5	343	2 T05221	hypothetical prote
18	86	9.5	420	2 B31104	LFY floral meriste
19	85.5	9.4	254	2 A31488	filaggrin - mouse
20	85	9.4	337	2 T49431	endorphine related
21	85	9.4	380	2 S51797	vasodilator-stimul
22	85	9.4	1095	2 T00329	hypothetical prote
23	84.5	9.3	134	2 T54810	pHL EIF1 - human
24	84.5	9.3	380	2 T24786	hypothetical prote
25	84.5	9.3	1159	2 I38465	probable potassium
26	84.5	9.3	1323	2 T00037	hypothetical prote
27	84.5	9.3	1562	2 T29146	hypothetical prote
28	84	9.3	270	1 WJH01C	homeotic protein H
29	84	9.3	313	2 A28444	filaggrin precurs

30 84 9.3 381 2 S16506 hypothetical prote
31 84 9.3 542 2 A44358 zixin - chicken
32 84 9.3 886 2 S07132 hypothetical prote
33 84 9.3 2023 2 T13154 polycomb protein e
34 83.5 9.2 625 2 A34615 profilaggrin - rat
35 83.5 9.2 672 2 T40333 tracheal colonizat
36 83.5 9.2 1215 2 T32734 myosin-IA - Acanth
37 83.5 9.2 1392 2 T51947 probable transcrip
38 83.5 9.2 3759 2 A35085 trithorax protein
39 83 9.2 263 1 E0BOA enkephalin e-12 pr
40 83 9.2 743 2 T09173 EH domain protein
41 83 9.2 760 2 T16726 hypothetical prote
42 82.5 9.1 523 2 T36677 probable secretory
43 82.5 9.1 558 2 A33616 heterogeneous ribo
44 82.5 9.1 635 2 T09648 nucleolin homolog
45 82.5 9.1 751 2 T02858 hypothetical prote

ALIGNMENTS

RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999

C:Accession: A55671

R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match 71.7%; Score 649; DB 2; Length 204;

Best Local Similarity 75.6%; Pred. No. 2.le-45;

Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSPAGSGKHHKQAPGLLDASHOQEQPTSSSH 60

Db 43 MFQIPFEPSEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRATNSH 97

Qy 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEEPSFPRGRSRAPPNLWAAQRYGRELRRMSDE 120

Db 98 HGGAGAMETRSRHSYPAGTDEDEGMEEELSFPFRGRSRAPPNLWAAQRYGRELRRMSDE 157

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168

Db 158 FEGSF-KGLPRPKSAGTATQMRQSGWTRIIQSWWDRNLGRGSGSTPSQ 204

RESULT 2

T42702

hypothetical protein DKFZp434F117.1 - human (fragment)

N:Alternate names: hypothetical protein DKFZp434B239.1

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000

C:Accession: T42702; T46502

R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: T22234

A:Accession: T42702

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-834 <AAA>

A:Cross-references: EMBL:AL133028

A:Experimental source: adult testis; clone DKFZp434F117

R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23029
A:Accession: T46502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 213-834 <AA2>
A:Cross-references: EMBL:AL137336
A:Experimental source: adult testis; clone DKFzp434B239
C:Genetics:
A:Note: DKFzp434F117.1; DKFzp434B239.1

Query Match 10.5%; Score 95; DB 2; Length 834;
Best Local Similarity 27.6%; Pred. No. 3.5;
Matches 50; Conservative 17; Mismatches 50; Indels 64; Gaps 11;

QY 13 EDSSSAERGLGSPSP---AGDGPSSGKHHKRAQAGLLWDASHQOEQTSSSHHGAGAVEI 69
Db 226 EEKKAEPAGENPPRGPGDARAGSK-----AKPQESPSSAS--ALAEWASI 272
QY 70 RSR-----HSSYPAGTDEDE-GMGEEPS-----FRGRSRSP-----NLWAAQRY--- 110
Db 273 RSLILNAESDPRSSERDQLRPQDETPRCGRDSRGKRTPPVNAKFSIMPAQKFSQ 332
QY 111 GRELRMSDEFVDSFKK-----GLPRKSAQTATOMROSSWTRVFQSWMDRLNLR 161
Db 333 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPAGV-----RELK 372
QY 162 G 162
Db 373 G 373

RESULT 3
T18396
erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fragm
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T18396
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi, T.
Cell 82, 77-87, 1995
A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen and
A:Reference number: Z18925; MUID:95330812
A:Accession: T18396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1729 <BAR>
A:Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1
C:Genetics:
A:Gene: EMP1
A:Note: var-2

Query Match 10.3%; Score 93.5; DB 2; Length 1729;
Best Local Similarity 21.6%; Pred. No. 10;
Matches 42; Conservative 23; Mismatches 66; Indels 63; Gaps 8;
QY 9 PSQEDSSAERGLGSPSP---AGDGPSSGKHHKRAQAGLL-----WDASHQOEQTSSSHH 61
Db 926 PSGNESPSPEKLPGQPTTETTKTPSSLLHAPVSPRLRRFLPW---HKFKQWKAQHG 982
QY 62 GGAGAVEIRSHSSYPAGTDEDEGMGEEPSFPRGRSRSPAPNLWAAQRY----- 110
Db 983 AGATGLQL-----PGVTVD-----SDPDQQLKRGKINPDLFQMFYTLGDRDICI 1031
QY 111 -----GRELRMSDEFVDSFKKGLPRKSAQTATOMROSSWTRVF--- 151
Db 1032 GGDRIIVGTIVSITGSESTKKKISIIIEGFLK-----KQTVTSPPROTSRTTPVHPQT 1086
QY 152 -----QSWMDRN 158
Db 1087 SVEKTPQQTWNEAN 1100

RESULT 4
T03166
probable immediate early protein - alcelaphine herpesvirus 1
C:Species: alcelaphine herpesvirus 1
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C:Accession: T03166
R:Ensser, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A:Reference number: Z14840; MUID:97404659
A:Accession: T03166
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1300 <ENS>
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AA58118.1; PID:g2338034
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 10.3%; Score 93; DB 2; Length 1300;
Best Local Similarity 29.0%; Pred. No. 8.3;
Matches 31; Conservative 6; Mismatches 56; Indels 14; Gaps 3;
QY 5 PEPESEQEDSSAERGLGP-SPAGDGPSSGKHHKRAQAGLLWDASHQOEQTSSSHHG 63
Db 466 PELEGEPERPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 521
QY 64 AGAVEIRSHSSYPAGTDEDEGMGEE-----PSPFGRSRSP 101
Db 522 EGPEGLEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPE 568

RESULT 5
T30757
hypothetical protein 155R - Molluscum contagiosum virus 1
N:Alternate names: MC155R
C:Species: Molluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 11-May-2000
C:Accession: T30757
R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host
A:Reference number: Z20876; MUID:96325459
A:Accession: T30757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <SEN>
A:Cross-references: EMBL:U60315; PIDN:AA55283.1
C:Genetics:
A:Note: MC155R

Query Match 10.2%; Score 92.5; DB 2; Length 336;
Best Local Similarity 30.6%; Pred. No. 2.1;
Matches 53; Conservative 17; Mismatches 68; Indels 35; Gaps 11;
QY 10 SEQEDSSAERGLGSPAGDGPSSGKHHKRAQAGLLWDASHQOEQTSSSHHGAGAVE 68
Db 118 SERERDGENRSAGPSSA---HSSGEYERASNEGRSSSCSRASEH---ESERSGSGS-E 171
QY 69 IRSRSHSSYPAGTDEDEGMGEEPSFPRG-----RSRSPAPNLWAAQRYGREL 115
Db 172 YQSALSAF-GGSEPSERSRG-LPPARGVPSCPAFQVWLDLLRSAGIN---AOLYAIEPE 226
QY 116 RMSDE-FVDSFKKGLPRKSAQTATOMROSSWTRVFQSWMDRLNLRGSSAPS 167
Db 227 SSSSETYSDS-----DSSDGGCGSRDRSLRSRGGQRYERNLS-GGSTPS 270

RESULT 6
A35938
profilaggrin - human (fragments)
C:Species: Homo sapiens (man)

Db 936 RAHRHQPSKEC ---AGAKGERRARHRGGPRAGPREAES -GEEPARRHRARHKAQP 987

JC5614
RNB6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change 05-Nov-1999
C:Accession: JC5614
R:Ohta, S.; Mineta, T.; Kimoto, M.; Tabuchi, K.
Biochem. Biophys. Res. Commun. 237, 307-312, 1997
A:Title: Differential display cloning of a novel rat cDNA (RNB6) that shows high expression
A:Reference number: JC5614; MUID:97415794
A:Accession: JC5614
A:Molecule type: mRNA
A:Residues: 1-393 <OHT>
A:Cross-references: GB:U0211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462
A:Experimental source: brain
C:Comment: This protein belongs to Ena/VASP family member, and is involved in the development of the brain.
1.

	Query Match	9.8%	Score 88.5;	DB 2;	Length 393;
	Best Local Similarity	28.2%;	Pred. No. 5.2;		
	Matches	40;	Conservative 16;	Mismatches 45;	Indels 41; Gaps 7;
Qy	13	EDSSAERGLGPGAGDGP	SGSGKHHQARGLLWDASHQEQPTSSHHGGAGAVETR	RSR	72
		:	:	:	:
Db	237	EDAS	-----GGSPSGTSGK-----DANR-----	ASSGGGGGGLMEEMNK	271
Qy	73	-----HSSVPAGTDE	DGEGMEP-----SPFRG-RRSAPPNLMWAAQRYGREL	RRMSD	119
		:	:	:	:
Db	272	LLAKRRKAAASQTDKPADRK	EDENQTEDPSISPGSGRATSQPPN	SSPAGRKPKWERSNSVE	331
Qy	120	EFVDSFKKGLPRK	SAGTATQM	141	
Db	332	KPVSSL---	LSRVKPGAGSVNDV	350	

RESULT 12

A44067

serine-rich protein hairless - fruit fly (*Drosophila melanogaster*)

N;Alternate names: 109K basic protein H

C;Species: *Drosophila melanogaster*

C;Date: 10-Jun-1993 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999

C;Accession: A44067; A58929; S33412; S24639

R;Bang, A.G.; Posakony, J.W.

Genes Dev. 6, 1752-1769, 1992

A;Title: The *Drosophila* gene Hairless encodes a novel basic protein that controls alternative splicing of the *Ultraviolet-B* gene

A;Reference number: A44067; MUID:92387549

A;Accession: A44067

A;Molecule type: DNA

A;Residues: 19-1077 <BAN>

A;Cross-references: GB:M95192; NID:gi57621; PID:gi57622

A;Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)

R;Preiss, A.

submitted to the EMBL Data Library, May 1994

A;Description: Hairless, a *Drosophila* gene involved in neural development, encodes a novel basic protein that controls alternative splicing of the *Ultraviolet-B* gene

A;Reference number: A58929

A;Accession: A58929

A;Molecule type: mRNA

A;Residues: 1-1077 <PRE>

A;Cross-references: EMBL:X67239; GB:S49642; NID:g578331; PID:g578332

R;Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.

Mech. Dev. 38, 143-156, 1992

A;Title: Hairless, a *Drosophila* gene involved in neural development, encodes a novel, serine-rich protein that controls alternative splicing of the *Ultraviolet-B* gene

A;Reference number: S33412; MUID:93041287

A;Accession: S33412

A;Molecule type: mRNA

A;Residues: 1-150, 'A', 152-701, 'LL', 704-890, 'R', 892-963, 'RLLP', 968-973, 975-1077 <MAI>

A;Cross-references: EMBL:X67239

C;Genetics:

A;Gene: FlyBase:H; hairless

A;Cross-references: FlyBase:FBgn0001169

Query Match 9.68; Score 86.5; DB 2; Length 1077;

	Best Local Similarity	28.9%;	Pred. No. 22;	Matches	37; Conservative	17; Mismatches	47; Indels	27; Gaps	7;
Qy	15	SSSERGLGSPACDGSG--SGKHHQRQAGLLWDASHOQEQTSSSHHGCGAGAVEIRSR	72	: :	:	:	:		
Db	678	SSSSSSG---KKCGDHPAAIISNVHHPQ-----HSMYQPSSSSYPRAL----	LTSP	721					
Qy	73	HSSYPAGTDEEGCEPESPFGRBSRAPPNLWNAQRYGRELRMSDEFVDSFKKGLPRP	132	: : : : : : :	:	:			
Db	722	KSPDVSGS--NGGGCKSPSTGTKKRPPYSAGSPVDYGHSFYR--DPYA-----GAGR	772						
Qy	133	KSAGTATQ	140						
Db	773	STGSASQ	780	: : :					

RESULT 13

S45252
SNF2beta protein - human

C:Species: Homo sapiens (man)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C:Accession: S45252

R:Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994

A:Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila br
A:Reference number: S45251; MUID:94268902

A:Accession: S45252

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1647 <CHI>

A:Cross-references: GB:D26156; NID:g505087; PIDN:BA051143.1; PID:g505088

C:Superfamily: unassigned bromodomain proteins; bromodomain homology

F:1485-1540/Domain: bromodomain homology <BRO>

[illegible]

```

RESULT 14
Tl3049
eye1id - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: Tl3049
R:Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z17592
A:Accession: Tl3049
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-2715 <TR>
A:Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1
C:Genetics:
A:Gene: eld
A:Cross-references: FlyBase:FBgn0003013
C:Function:
A:Description: could act as a transcription factor antagonistic to the wg pathway
C:Keywords: DNA binding

```

Query Match	9.6%	Score 86.5;	DB 2;	Length 2715;
Best Local Similarity	25.8%;	Pred. No. 61;		
Matches 41;	Conservative	11;	Mismatches 48;	Indels 59;
Matches 10;				Gaps 10;

```

Qy 8 EPSEQEDSSAERGLG-PSPACDGPSSGKKHHRQAPG-----LLWDASHQEQRP----- 55
      :|| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 54 DPISIQQQNVAPHPYGAPPPPGSGGG-----PPGPDPAAMVHYHLHQOQQQHPPPP 106
      :|| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 56 --TSSHHGGAGAVERSHSSYPAGT-EDDEGMGEE-----PSPFGRSRSAPPNL 104
      :|| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 HMQQQQHHGGPAPP-----PGGAPEHAPGVKEETHLPHPHPAYGRYH-ADPNM 157
      :|| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 105 WAAQRYGRELRRMSDEFVDSFKKGLPRPKSAGTATQMRQ 143
      :|| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 158 -----DPRYQGQLP--GGKPPQQQQ 176
      :|| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
T43500
hypothetical protein DKFp586G172l.1 - human (fragment)
C:Species: Homo sapiens (man)
C:date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43500
R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A:reference number: Z22515
A:Accession: T43500
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-222 <AAA>
A:Cross-references: EMBL:AL133642
A:Experimental source: adult uterus; clone DKFp586G172l
C:Genetics:
A:Note: DKFp586G172l.1

```

```

Query Match          9.5%; Score 86; DB 2; Length 222;
Best Local Similarity 27.3%; Pred. No. 4.4;
Matches 41; Conservative 15; Mismatches 56; Indels 38; Gaps
6;

QY 13 EDSSAERGLGSPAGDGPSCSGKHRRQAPGLLWDASHQQEQPTSSSHHGAGAVEIRSR 72
      |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 77 EDAS-----GGSSPSTSKS-----DNR-----ASSCGGGGLMEENK 111
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:

QY 73 -----HSSYPAGTDEDEGMGEEP--SPFRG-RSRAPPNLWAAQRYGRELRRMSD 119
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 112 LLAKRRRAAQSQDPAEKKEDESQMEDPSTPSTCTRAASOPPNSSSEAGRKPWERSNVS 171
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:

QY 120 EFVDSFKGLPRPKSAGTATQMRQSSSWTR 149
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:
Db 172 KPVSSIISRTPSVAKSPKAPKSPLOSQPHSR 201
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:

```

Search completed: October 9, 2001, 15:54:03
Job time: 233 sec


```
QY 121 FVDSFKKGLPRKSGACTATQMQRSSWTRVFSQWMDNLRGSSAPSQ 168
|||||
Db 121 FVDSFKKGLPRKSGACTATQMQRSSWTRVFSQWMDNLRGSSAPSQ 168

RESULT 2
BAD_MOUSE STANDARD; PRT; 204 AA.
AC Q61337;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
GN BAD OR BGC6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Thymus;
RX MEDLINE=95136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
RL Cell 80:285-291(1995).
CC -!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE
CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL
CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
CC -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
CC BAX, MCL-1, A1, OR BCL-X(S).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL; L37296; AAA64465.1;
DR MGD; MGI:1096330; Bad.
KW Apoptosis. 138 158 BH1.
FT DOMAIN 182 199 BH2.
SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 71.7%; Score 649; DB 1; Length 204;
Best Local Similarity 75.6%; Pred. No. 1.7e-42;
Matches 127; Conservative 12; Mismatches 22; Indels 6; Gaps 3;

QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPGSGKGHHKRAQPLGLWDASHQEQPTSSSH 60
|||||
Db 43 MFQIPEFSEQEDASATRGGLSLTEQDP---GPY--LAPGLGSLNHQGRATNSH 97
|||||

QY 61 HGGAGAVEIRSHSSYPAGTEDEGMEGPEPSPPGRKRSAPPNLNAAQRYGRELRRMSDE 120
|||||
Db 98 HGGAGAMETRSRSHSSYPAGTEDEGMEELSPPFRGRSAPPNLNAAQRYGRELRRMSDE 157
|||||

QY 121 FVDSFKKGLPRKSGACTATQMQRSSWTRVFSQWMDNLRGSSAPSQ 168
|||||
Db 158 FEGSF-KGLPRKSGACTATQMQRSGAGWTRIIQSWMDNLRGSGSPSQ 204
|||||

RESULT 3
CCAA_HUMAN STANDARD; PRT; 2505 AA.
ID CCAA_HUMAN
```

CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; BI-1/1A-2, BI-1(V1),
 CC BI-1-GGCAG/1A-1 (SHOWN HERE), BI-1(V1)-GGCAG, BI-1(V2), BI-1(V2)-
 CC GGCAG AND BI-1(V2.V3). ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC; MAINLY FOUND IN CEREBELLUM,
 CC CEREBRAL CORTEX, THALAMUS AND HYPOTHALAMUS. NO EXPRESSION IN
 CC HEART, KIDNEY, LIVER OR MUSCLE. PURKINJE CELLS CONTAIN
 CC PREDOMINANTLY P-TYPE VSCC. THE Q-TYPE BEING A PROMINENT CALCIUM
 CC CURRENT IN CEREBELLAR GRANULE CELLS.

CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- POLYMORPHISM: THE POLY-GLN REGION OF CACNA1A IS POLYMORPHIC: 6 TO
 CC 17 REPEATS IN THE NORMAL POPULATION, EXPANDED TO ABOUT 21 TO 30
 CC REPEATS IN SPINOCEREBELLAR ATAXIA 6 (SCA6) PATIENTS. THERE SEEMS
 CC TO BE A CORRELATION BETWEEN THE REPEAT NUMBER AND EARLIER ONSET OF
 CC THE DISORDER.

CC -1- DISEASE: EXPANSION OF A CAG REPEAT IN THE CODING REGION OF CACNA1A
 CC IS THE CAUSE OF ONE FORM OF SPINOCEREBELLAR ATAXIA 6 (SCA6). AN
 CC AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY SLOWLY PROGRESSIVE
 CC CEREBELLAR ATAXIA OF THE LIMBS AND GAIT, DYSPHAGIA, NYSTAGMUS,
 CC AND MILD VIBRATORY AND PROPRIOCEPTIVE SENSORY LOSS. THESE SYMPTOMS
 CC ARE PROBABLY EXPLAINED BY SEVERE LOSS OF CEREBELLAR PURKINJE
 CC CELLS.

CC -1- DISEASE: DEFECTS IN CACNA1A ARE THE CAUSE OF FAMILIAL HEMIPLEGIC
 CC MIGRAINE (FHM). ALSO KNOWN AS MIGRAINE FAMILIAL HEMIPLEGIC 1
 CC (MHP1), EPISODIC ATAXIA TYPE 2 (EA-2), ACETAZOLAMIDE-RESPONSIVE
 CC HEREDITARY PAROXYSMAL CEREBELLAR ATAXIA (APCA), AND POSSIBLY OTHER
 CC COMMON TYPES OF MIGRAINES. FHM, A RARE AUTOSOMAL DOMINANT SUBTYPE
 CC OF MIGRAINE WITH AURA, IS ASSOCIATED WITH ICTAL HEMIPARESIS AND,
 CC IN SOME FAMILIES, PROGRESSIVE CEREBELLAR ATROPHY. EA-2 IS ANOTHER
 CC AUTOSOMAL DOMINANT PAROXYSMAL CEREBRAL DISEASE, CHARACTERIZED BY
 CC ACETAZOLAMIDE-RESPONSIVE ATTACKS OF CEREBELLAR ATAXIA AND
 CC MIGRAINE-LIKE SYMPTOMS, INTERICTAL NYSTAGMUS, AND CEREBELLAR
 CC ATROPHY.

CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.

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CC -----
 CC EMBL: AF004884; AAB61613.1; -
 CC EMBL: AF004883; AAB61612.1; -
 CC EMBL: X9897; CAA68172.1; -
 CC EMBL: 280114; -; NOT_ANNOTATED_CDS.
 CC EMBL: 280115; -; NOT_ANNOTATED_CDS.
 CC EMBL: U79666; AAB64179.1; -
 CC EMBL: U79666; AAB49674.1; ALT_INIT.
 CC EMBL: U79664; AAB49675.1; ALT_INIT.
 CC EMBL: U79665; AAB49676.1; ALT_INIT.
 CC EMBL: U79667; AAB49677.1; ALT_INIT.
 CC EMBL: U79668; AAB49678.1; ALT_INIT.
 CC EMBL: S76537; AAB33068.1; -
 CC EMBL: U06702; -; NOT_ANNOTATED_CDS.
 CC MIM: 601011; -
 CC MIM: 183086; -
 CC MIM: 141500; -
 CC InterPro: IPR000636; -
 CC InterPro: IPR002077; -
 CC Pfam: PF00520; Ion_trans; 4.

DR PRINTS; PR00167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
 KW Disease mutation; triplet repeat expansion.
 FT REPEAT 85 363 I.
 FT REPEAT 473 717 II.
 FT REPEAT 1231 1514 III.
 FT REPEAT 1551 1814 IV.
 FT DOMAIN 1 98 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 99 117 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 118 135 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 136 155 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 156 167 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 168 185 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 186 190 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 191 209 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 210 228 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 229 248 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 249 335 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 336 360 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 361 487 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 488 506 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 507 521 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 522 541 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 542 549 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 550 568 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 569 578 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 579 597 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 598 616 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 617 636 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 637 689 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 690 714 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 715 1242 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1243 1261 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1262 1277 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1278 1297 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1298 1309 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1310 1328 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1329 1339 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1340 1358 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1359 1377 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1378 1397 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1398 1484 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1485 1509 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1510 1564 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1565 1593 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1594 1598 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1599 1618 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1619 1626 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1627 1645 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1646 1652 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1653 1671 S4 OF REPEAT IV (POTENTIAL).

Query Match 10.7%; Score 97; DB 1; Length 2505;

Best Local Similarity 23.5%; Pred. No. 6.9;

Matches 48; Conservative 22; Mismatches 54; Indels 80; Gaps 11;

QY 5 PEPEPSEQD-----SSAERGLGSP---ACDGPSSGSKHROAP----- 42
 Db 2313 PQQQQQQQQQQAVARPGRAATSGPRYPGPTABPLAGDRPPTGGTSGSRPMRVRPG 2372
 QY 43 -----GLWDAS--HQEQPTSSHHGGAGAVEIRSHHSYPAGTDEDE--- 84
 Db 2373 PARSESPRACHGGRWPASGPHVSEGGPPGRHHG-----YRGSYDEADG 2419
 QY 85 ---GMGE-----PSPFR-----GRS-----RSAPPLWAAQRYGRLRMSDEFV 122
 Db 2420 PGSGGGEAMAGAYDAPPVVRHASSGATGRSPRTPRASGPACASPSRHG----RLPNGY 2476
 QY 123 DSPKKGLPRKSGAGTATQMRQSSS 146
 Db 2477 PA--HGLARPGGSRKGLHEPS 2498

```
RESULT 4
CYAA_NEUCR STANDARD; PRT: 2300 AA.
ID Q01631;
AC 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLATE
CYCLASE).
GN CR-1 OR NAC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RX MEDLINE=92000795; PubMed=1680356;
RA Kore-Eda S., Murayama T., Uno I.;
RT "Isolation and characterization of the adenylate cyclase structural
gene of Neurospora crassa.";
RL Jpn. J. Genet. 66:317-334(1991).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
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CC -----
DR EMBL; D00909; BAA00755.1; -
DR InterPro; IPR001611; -
DR InterPro; IPR001932; -
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PRO00019; LEURICHRPT.
DR PROSITE; PS50125; GUANYLATE CYCLASES.2; 1.
KW Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT REPEAT 867 990
FT REPEAT 892 914
FT REPEAT 915 938
FT REPEAT 938 961
FT REPEAT 962 986
FT REPEAT 988 1008
FT REPEAT 1009 1031
FT REPEAT 1033 1055
FT REPEAT 1056 1079
FT REPEAT 1081 1097
FT REPEAT 1098 1120
FT REPEAT 1122 1142
FT REPEAT 1143 1165
FT REPEAT 1166 1188
FT REPEAT 1189 1211
FT REPEAT 1213 1234
FT REPEAT 1349 1369
FT REPEAT 1398 1420
FT REPEAT 1422 1445
FT REPEAT 1447 1469
FT REPEAT 1474 1497
FT REPEAT 1513 1538
FT REPEAT 1564 1829
FT DOMAIN 1830 2300
FT DOMAIN 49 52
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FT DOMAIN 204 221 POLY-GLN.
SQ SEQUENCE 2300 AA; 254752 MW; 52E79B90E6B17A7B CRC64;

Query Match 10.4%; Score 94.5; DB 1; Length 2300;
Best Local Similarity 24.2%; Pred. No. 9.7;
Matches 51; Conservative 23; Mismatches 74; Indels 63; Gaps 11;

QY 17 SAERGLGSPAGDGPSSGCKHHR---QAPGLLDASHOEOPTSSSHH-----GGAGAV 67
Db 343 SSEISL-PPSHSGPMSTGKHSYSLPGS--GRSHDRNYSNATDHHPTFGSVSTV 399

QY 68 EIRSRHSS-----YPA-----GTEDECMGEEP-----SPFRGR---SRSA 100
Db 400 GGRDRDASPVPSPRPPTVPAPVPEVVPVLYQEAADDIARYGEAPVTSLTGPDORDYIDSSQN 459

QY 101 PPNLWAAQRYGREL-----RRMSDFVDSFKGLPRKPSAGT-----AT 139
Db 460 PPKTSSARSAGHSIVHLPGHHKHNKSNEDPRALKPSLSREDSAAFPARFNGSSMMGT 519

QY 140 OMRQSS---SWTRVFQSWDRNLGRGSSAPS 167
Db 520 RSRAQSPAPSWTGTSGRLKANSISDGTSPA 550

RESULT 5
SGL_BOVIN STANDARD; PRT: 646 AA.
ID SGL_BOVIN
AC P23389; O02707;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DE SECRETAGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
DE PEPTIDE; SECRETOLYTIN].
GN CHGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal chromaffin;
RX MEDLINE=91223091; PubMed=2025642;
RA Bauer J.W., Fischer-Colbrie R.;
RT "Primary structure of bovine chromogranin B deduced from cDNA
sequence.";
RL Biochim. Biophys. Acta 1089:124-126(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=97282588; PubMed=9136897;
RA Yoo S.H., Kang Y.K.;
RT "Identification of the secretory vesicle membrane binding region of
chromogranin B.";
RL FEBS Lett. 406:259-262(1997).
RN [3]
RP SEQUENCE OF 21-646 FROM N.A.
RC TISSUE=Adrenal medulla;
RA Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J.,
RA Thomas G., Clivelli O., Viveros O.H.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 634-646.
RC TISSUE=Adrenal chromaffin;
RX MEDLINE=95262699; PubMed=7744058;
RA Strud J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
RA van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
RT "Processing of chromogranin B in bovine adrenal medulla.
RT Identification of secretolysin, the endogenous C-terminal fragment of
RT residues 614-626 with antibacterial activity.";
RL Eur. J. Biochem. 229:356-368(1995).
RN [5]
```



```

RP CHARACTERIZATION OF SECRETOLYTIN.
RX MEDLINE=96184581; PubMed=8603705;
RA Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutigue M.-H.;
RT "Antibacterial activity of secretolytin, a chromogranin B-derived
RL peptide (614-626), is correlated with peptide structure.";
RL FEBS Lett. 379:273-278(1996).
CC -!- FUNCTION: SECRETOLYTIN I IS A NEUROENDOCRINE SECRETORY GRANULE
CC PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE
CC PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS
CC SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.
CC -!- FUNCTION: SECRETOLYTIN HAS ANTIBACTERIAL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
CC GRANULES.
CC -!- PTM: O-GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE CHROMOGANIN / SECRETOGANIN PROTEIN
CC FAMILY.
CC
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DR EMBL; X55027; CAA38846.1; -.
DR EMBL; U88551; AAC48720.1; -.
DR EMBL; X55489; CAA39109.1; -.
DR PIR; S15901; S15901.
DR InterPro; IPR001819; -.
DR InterPro; IPR001990; -.
DR Pfam; PF01271; Granin; 1.
DR PRINTS; PR00659; CHROMOGANIN.
DR PROSITE; PS00422; GRANINS.1; 1.
DR PROSITE; PS00423; GRANINS.2; 1.
KW Sulfatation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT CHAIN 21 646
FT PEPTIDE 418 484
FT PEPTIDE 634 646
FT DISULFID 36 57
FT MOD_RES 158 158
FT MOD_RES 315 315
FT CONFLICT 64 64
FT CONFLICT 70 70
FT CONFLICT 93 98
FT CONFLICT 181 181
FT CONFLICT 261 261
FT CONFLICT 386 386
FT CONFLICT 481 481
FT CONFLICT 597 597
FT CONFLICT 646 646
SQ SEQUENCE 646 AA; 73339 MW; 420DB1178FD9E415 CRC64;

Query Match 9.9%; Score 90; DB 1; Length 646;
Best Local Similarity 28.7%; Pred. No. 5.7;
Matches 37; Conservative 16; Mismatches 52; Indels 24; Gaps 6;

Qy 9 PSEQDSSSAERGLGSPAGDPSGSKHH--RQAPGLLDASHQEQEP--TSSSHHCGA 64
Db 246 PGESEDA-----SPEVDKRHSRPHRHGSRP-----DRSQEGNPLEESHVGTG 293
Qy 65 GAVETRSRHSYPAGTDEGMEGPEPSFRGRSRSAPNLAAQRYGR-----ELRRMS 118
Db 294 NSDEKARHPAHPFALESCAEGVEVR--RHSAQAQPDLOGARFGGGRGEGHQAALRRPS 351
Qy 119 DEFVDSFKK 127
Db 352 BESLEQENK 360

RESULT 6
CCAB_HUMAN

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ID CCAB_HUMAN STANDARD; PRT; 2339 AA.
AC Q00975;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
DE III) (BIIT).
GN CACNA1B OR CACNL1A5 OR CACH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).
RC TISSUE=Brain;
RX MEDLINE=92335886; PubMed=1321501;
RA Williams M.E., Brust P.F., Feldman D.H., Patthi S., Simerson S.,
RA Maroufi A., McCue A.F., Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of an omega-conotoxin-sensitive
RT human N-type calcium channel.";
RL Science 257:389-395(1992).
RN [2]
RP SEQUENCE OF 1-94 FROM N.A.
RC TISSUE=Lung fibroblast;
RA Kim D.S., Jung H.H., Park S.H., Chin H.;
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CIX-GVIA) AND BY OMEGA-AGATOXIN-
CC IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO
CC DIHYDROPYRIDINES (DHP), AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
CC DIRECTED MIGRATION OF IMMATURE NEURONS.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1B-1 (SHOWN HERE) AND
CC ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE
CC CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.
CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC -!- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC FAMILY.
CC
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CC
CC -----
DR EMBL; M94172; AAA51897.1; -.
DR EMBL; M94173; AAA51898.1; -.
DR EMBL; U76666; AAC51138.1; -.
DR MIM; 601012; -.

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DR InterPro: IPR000636; --
DR InterPro: IPR002077; --
DR Pfam: PF00520; ion_trans. 4.
DR PRINTS: PR00167; CACHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Calcium channel; Glycoprotein; Repeat; Multigene family;
KW Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.
FT REPEAT 82 359 I.
FT REPEAT 468 712 II.
FT REPEAT 1137 1419 III.
FT REPEAT 1456 1711 IV.
FT DOMAIN 1 95
FT TRANSMEM 96 114
FT DOMAIN 115 132
FT TRANSMEM 133 152
FT DOMAIN 153 163
FT TRANSMEM 164 183
FT DOMAIN 184 187
FT TRANSMEM 188 206
FT DOMAIN 207 225
FT TRANSMEM 226 245
FT DOMAIN 246 331
FT TRANSMEM 332 356
FT DOMAIN 357 482
FT TRANSMEM 483 501
FT DOMAIN 502 516
FT TRANSMEM 517 536
FT DOMAIN 537 544
FT TRANSMEM 545 562
FT DOMAIN 563 573
FT TRANSMEM 574 592
FT DOMAIN 593 611
FT TRANSMEM 612 631
FT DOMAIN 632 684
FT TRANSMEM 685 709
FT DOMAIN 710 1151
FT TRANSMEM 1152 1169
FT DOMAIN 1170 1185
FT TRANSMEM 1186 1205
FT DOMAIN 1206 1217
FT TRANSMEM 1218 1236
FT DOMAIN 1237 1246
FT TRANSMEM 1247 1265
FT DOMAIN 1266 1284
FT TRANSMEM 1285 1304
FT DOMAIN 1305 1391
FT TRANSMEM 1392 1416
FT DOMAIN 1417 1471
FT TRANSMEM 1472 1490
FT DOMAIN 1491 1505
FT TRANSMEM 1506 1525
FT DOMAIN 1526 1533
FT TRANSMEM 1534 1552
FT DOMAIN 1553 1563
FT TRANSMEM 1564 1582
FT DOMAIN 1583 1601
FT TRANSMEM 1602 1621
FT DOMAIN 1622 1693
FT TRANSMEM 1684 1708
FT DOMAIN 1709 2339
FT TRANSMEM 2050 2094
FT DOMAIN 2118 2122
FT TRANSMEM 379 396
FT NP_BIND 451 458
FT SITE 314 314
FT SITE 663 663
FT SITE 1365 1365
FT SITE 1655 1655

FT MOD_RES 1719 1719 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT CALBIND 1737 1748 BY SIMILARITY.
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1563 1563 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 2164 2339 GSGVNGSPLSTSGASTPGRRGRQLPOTPLTPRPSITYK
FT QPLAPGSRIGDYLQRLDSEASVHALPDLTFEEAVAT
FT NSGRSRSTYSVSLTSQSHPLRRVPGVHCTGLGLSGGRAR
FT HSYHPDDODHMC -> AGSAVGFPNTPCCRETPTSPSPWPL
FT ALEALALTWGSVWTVRPLSTPCLSTRSLRRLWPPTRAAP
FT POLPTCPP (IN ISOFORM ALPHA-1B-2).
SQ SEQUENCE 2339 AA; 262494 MW; 17A45C6D1E76B39D CRC64;
Query Match 9.9%; Score 90; DB 1; Length 2339;
Best Local Similarity 30.8%; Pred. No. 21;
Matches 36; Conservative 16; Mismatches 35; Indels 30; Gaps 9;
QY 8 EPSEQED-----SSAERGLGSPSA-----GDGPSGKGKHHQAPGLLWDA----- 48
Db 878 EPGAREPRPHRSKSKAAGPPEARSGRGPBGRRHRR--GSPEAAERPRRH 935
QY 49 -SHQEQPTSSHHGGAGAV-EIRSRHSYP-AGTEDDEGMGEPS-PFRGRSRAP 101
Db 936 RAHRHODPSKEC-----AGAKGERARRHGRGPRAGPREAES-GEPPARRHRAKQOP 987
RESULT 7
IE18_PRIVIF STANDARD; PRT; 1461 AA.
AC P11675;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE IMMEDIATE-EARLY PROTEIN IE180.
GN IE.
OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=31523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89315207; PubMed=2546124;
RA Cheung A.K.;
RT "DNA nucleotide sequence analysis of the immediate-early gene of
RT pseudorabies virus."
RL Nucleic Acids Res. 17:4637-4646(1989).
RN [2]
RP REVISIONS.
RA Cheung A.K.;
RL Submitted (NOV-1989) to the EMBL/GenBank/DDAJ databases.
CC -!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
CC -!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
CC -!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
CC PHOSPHORYLATION.
CC -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
CC -----
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CC -----
DR EMBL; X15120; CA33214.1; -
DR PIR; S04713; EDSEIF.
KW Early protein; Transcription regulation; Trans-acting factor;
KW DNA-binding; Phosphorylation; Nuclear protein.
FT DOMAIN 390 405 POLY-SER.

FT DOMAIN 958 966 POLY-SER.
SQ SEQUENCE 1461 AA; 149833 MW; 7F31E7ABE403B208 CRC64;

Query Match 9.9%; Score 89.5; DB 1; Length 1461;
Best Local Similarity 29.4%; Pred. No. 14;
Matches 50; Conservative 9; Mismatches 70; Indels 41; Gaps 8;

QY 9 PSEQDSSSAERGLGP--SPAGDG-PSGS---GKHRO-----APGLLWD 47
I: : : | | : | : | | | | | : | | |
DB 231 PARRGFASPAAGVAPAGGGGAPGGGDRHHHGHREPLLEPAARLRDPRPLGA 290
QY 48 ASHQEQPTSSHHGGAGAVEIRSHSSYPAGTEDE-----GMGEPPSPFRGRSRGAP 101
I: | | | | | | | | | | : | | | : | | |
DB 291 RSPVSSNPNSSSSSTTTVAVEPVAR-----GPEKDEGLGLAGDGAPLQRPQRRRAG 344
QY 102 PNLAAQRYGRELRLMSDEFVDS-----FKKGLPRPKAGTATQMRQSSS 146
I: | | | | | | | | | | : | | | : | | |
DB 345 E---GALRRGRGFSSSGSDSLSPARSPAPRAPAAAAARRRSASS 391

RESULT 8

CMGA_BOVIN STANDARD; PRT; 449 AA.
ID CMGA_BOVIN
AC P05059; P79392;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CHROMOGRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN I) (SP-I)
DE [CONTAINS: VASOSTATIN-1; CHROMOSTATIN; CHROMACIN; PANCREASTATIN; WE-
14; CATESTATIN].
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92140395; PubMed=1779968;
RA Iacangelo A.L., Grimes M., Eiden L.E.;
RT "The bovine chromogranin A gene: structural basis for hormone
RT regulation and generation of biologically active peptides.";
RL Mol. Endocrinol. 5:1651-1660(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86300648; PubMed=3755681;
RA Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J.,
RA Mallet J., Huttner W.B.;
RT "The primary structure of bovine chromogranin A: a representative of
RT a class of acidic secretory proteins common to a variety of
RT peptidergic cells.";
RL EMBO J. 5:1495-1502(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86311345; PubMed=3018587;
RA Iacangelo A., Afritter H.-U., Eiden L.E., Herbert E., Grimes M.;
RT "Bovine chromogranin A sequence and distribution of its messenger RNA
RT in endocrine tissues.";
RL Nature 323:82-86(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260925; PubMed=3474638;
RA Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
RA Levine M.A.;
RT "Primary structure of bovine pituitary secretory protein I
RT (chromogranin A) deduced from the cDNA sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97228583; PubMed=9074643;
RA Kang Y.K., Yoo S.H.;
RT "Identification of the secretory vesicle membrane binding region of

chromogranin A.";
RL FEBS Lett. 404:87-90(1997).
RN [6]
RP SEQUENCE OF 19-45, AND CALCIUM-BINDING.
RX MEDLINE=90354431; PubMed=2387861;
RA Yoo S.H., Albanesi J.P.;
RT "Ca2(+)-induced conformational change and aggregation of chromogranin
RT A.";
RL J. Biol. Chem. 265:14414-14421(1990).
RN [7]
RP SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
RX MEDLINE=91142185; PubMed=1996343;
RA Galindo E., Rill A., Bader M.-F., Anis D.;
RT "Chromostatin, a 20-amino acid peptide derived from chromogranin A,
RT inhibits chromaffin cell secretion.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
RN [8]
RP ERRATUM.
RA Galindo E., Rill A., Bader M.-F., Anis D.;
RL Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
RN [9]
RP SEQUENCE OF 266-312.
RX MEDLINE=89331945; PubMed=2756155;
RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,
RA Chang D., Tatemoto K.;
RT "Isolation and characterization of bovine pancreastatin.";
RL Regul. Pept. 25:207-213(1989).
RN [10]
RP SEQUENCE OF 191-212 (CHROMACIN).
RC TISSUE-Chromaffin granules;
RX MEDLINE=97067080; PubMed=8910482;
RA Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,
RA van Dorsselaer A., Anis D., Metz-Boutigue M.-H.;
RT "Antibacterial activity of glycosylated and phosphorylated
RT chromogranin A-derived peptide 173-194 from bovine adrenal medullary
RT chromaffin granules.";
RL J. Biol. Chem. 271:28533-28540(1996).
RN [11]
RP CHARACTERIZATION OF CATESTATIN.
RX MEDLINE=97439785; PubMed=9294131;
RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,
RA Gill B.M., Farmer R.J.;
RT "Novel autocrine feedback control of catecholamine release. A discrete
RT chromogranin A fragment is a noncompetitive nicotinic cholinergic
RT antagonist.";
RL J. Clin. Invest. 100:1623-1633(1997).
RN [12]
RP CHARACTERIZATION OF CATESTATIN.
RX MEDLINE=99000113; PubMed=9786174;
RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
RT "Mechanism of cardiovascular actions of the chromogranin A fragment
RT catestatin in vivo.";
RL Peptides 19:1241-1248(1998).
RN [13]
RP 3D-STRUCTURE MODELING OF CATESTATIN.
RX MEDLINE=99025667; PubMed=9809795;
RA Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
RA Khan I., Farmer R.J., O'Connor D.T.;
RT "Mechanism of action of chromogranin A on catecholamine release:
RT molecular modeling of the catestatin region reveals a beta-
RT strand/loop/beta-strand structure secured by hydrophobic interactions
RT and predictive of activity.";
RL Regul. Pept. 77:43-53(1998).
RN [14]
RP CHARACTERIZATION OF VASOSTATIN-1.
RX MEDLINE=20219105; PubMed=10753865;
RA Lugardon K., Raftery R., Goumon Y., Corti A., Delmas A., Bulet P.,
RA Anis D., Metz-Boutigue M.-H.;
RT "Antibacterial and antifungal activities of vasostatin-1, the N-
RT terminal fragment of chromogranin A.";
RL J. Biol. Chem. 275:10745-10753(2000).
RN [15]
RP CARBOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.

Matches	37;	Conservative	16;	Mismatches	51;	Indels	55;	Gaps	6;
---------	-----	--------------	-----	------------	-----	--------	-----	------	----

Qy	9	PSEQEDSSAERGLGSPAGDPGSGKHHKQAPGLWDASHQ	-----	51
		:		
Db	347	PSQENSESQAELHES-RGNDPNATSHSRE	-----	ROADSESSEEDVLDKPDS 396
Qy	52	-----QEQPTSSSHHGAGAVEIRSRUSSIYPAGTDEDDGMCGEPSFPRGRSRAPPNLWA 106		
		:		
Db	397	ESTSTEEQADSEHSHE-----SLRSEES-PESTEEQNSSQEQAGTQSRQESP	-----	444
Qy	107	AQRYGRELRLRMDSFVDSFKKGLPRPKSAGTATOMROSS 145		
		: :		
Db	445	-----SEDDGSDSDSRKSDSNSTSVSSS 472		

RESULT	10
HLES_DROME	
ID	HLES_DROME
AC	002308; STANDARD; PRT; 1077 AA.
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	01-FEB-1994 (Rel. 28, Last annotation update)
DE	HAIRLESS PROTEIN.
GN	H.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;
RI	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=92387549; PubMed=1516831;
RA	Bank A.G., Posakony J.W.;
RA	"The Drosophila gene Hairless encodes a novel basic protein that
RT	controls alternative cell fates in adult sensory organ development. ";
RT	Genes Dev. 6:1752-1769(1992).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=93041287; PubMed=1419850;
RA	Maier D., Stumm G., Kuhn K., Preiss A.;
RA	"Hairless, a Drosophila gene involved in neural development, encodes
RT	a novel, serine rich protein. ";
RT	Mech. Dev. 38:143-156(1992).
RL	
CC	-!- FUNCTION: IS A POTENT ANTAGONIST OF NEUROGENIC GENE ACTIVITY
CC	DURING SENSORY ORGAN DEVELOPMENT. THE EXPRESSION OF DISTINCT CELL
CC	FATES BY THE TRICHOGEN (SHAFT) / TORMOGEN (SOCKET) SISTER CELL
CC	PAIR DEPENDS ON THE LEVEL OF H ACTIVITY. A CERTAIN THRESHOLD LEVEL
CC	OF H ACTIVITY IS REQUIRED, BELOW WHICH BOTH SISTER CELLS ADOPT THE
CC	TORMOGEN FATE.
CC	-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC	-!- TISSUE SPECIFICITY: OVARY, EMBRYOS, LARVAL AND PUPAL IMAGINAL
CC	DISCS.
CC	-!- SIMILARITY: CONTAINS A "PRD MOTIF".
CC	-----
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CC	-----
DR	EMBL; M95192; AAA28607.1; ALT_INIT.
DR	EMBL; X67239; CAA47664.1; -
DR	HSPP; P04002; IWFA.
DR	FlyBase; FBgn0001169; H.
KW	Developmental protein; Nuclear protein; DNA-binding.
FT	DOMAIN 115 123 THR-RICH.
FT	DOMAIN 642 648 POLY-SER.
FT	DOMAIN 879 891 POLY-ALA.
FT	DOMAIN 937 946 POLY-ALA.
FT	DOMAIN 964 974 ALA-RICH.
FT	DOMAIN 979 1008 HIS/PRO-RICH (PRD MOTIF).

CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
CC -----
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CC -----
DR EMBL: U29175; AAB40977.1; -.
DR EMBL: D26156; BAA05143.1; -.
DR EMBL: AC006127; AAC97987.1; -.
DR MIM: 603254; -.
DR InterPro: IPR000330; -.
DR InterPro: IPR001487; -.
DR InterPro: IPR001650; -.
DR Pfam: PF00176; SNF2_N; 1.
DR Pfam: PF00439; bromodomain; 1.
DR Pfam: PF00271; helicase_C; 1.
DR PRINTS: PR00503; BROMODOMAIN.
DR PROSITE: PS00633; BROMODOMAIN_1; 1.
DR PROSITE: PS0014; BROMODOMAIN_2; 1.
KW Transcription regulation; Nuclear protein; Activator; Bromodomain;
FT ATP-binding; Helicase.
FT DOMAIN 578 588 POLY-LYS.
FT DOMAIN 663 672 POLY-GLU.
FT NP_BIND 779 786 ATP (POTENTIAL).
FT SITE 881 884 DEGH BOX.
FT DOMAIN 1360 1364 POLY-GLU.
FT DOMAIN 1477 1547 BROMODOMAIN.
FT DOMAIN 1571 1584 POLY-GLU.
FT SEQUENCE 1647 AA; 184585 MW; 78785E7953277FID CRC64;

Query Match 9.6%; Score 86.5; DB 1; Length 1647;
Best Local Similarity 29.8%; Pred. No. 27;
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;
QY 9 PSQEDSSAERGIGSPAGDPSGSGKHH--RQAP-GLLWDASHQEQPTSSSHHGA 64
DB 30 PSCGSPGSAHSMWGSP---GPSSAG--HPITQGGYPQDNMHQMKPMESHEKGM 84
QY 65 GAVEIRSRHSSYPAGTDDDEGMGEPSFPRGRSRAPPNLAQAQ 108
DB 85 SDDPRYNQKMGMRSGGHAGMGPPSPMDQHSQGYPSPLGGSE 128

RESULT 12
ID HXA5_MOUSE STANDARD; PRT; 270 AA.
AC P09021;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HOMEBOX PROTEIN HOX-A5 (HOX-1.3) (M2).
GN HOXA5 OR HOXA-5 OR HOX-1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=88056292; PubMed=2890554;
RA Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr.,
RA Tani M., Lazzarini R.A.;
RT "Expression of a homeo domain protein in noncontact-inhibited
RL cultured cells and postmitotic neurons.";
RN Genes Dev. 1:482-496(1987).
RX SEQUENCE FROM N.A.
RX MEDLINE=88328807; PubMed=2901335;

RA Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labeit S.,
RA Lehrach H., Gruss P.;
RT "Coding sequence and expression of the homeobox gene Hox 1.3.";
RL Development 102:349-359(1988).
RN [3]
DNA-BINDING SPECIFICITY.
RP MEDLINE=89232713; PubMed=2565857;
RX Odenwald W.F., Garbern J., Arnheiter H., Tournier-Lasserre E.,
RA Lazzarini R.A.;
RT "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
RT phosphoprotein.";
RN Genes Dev. 3:158-172(1989).
RL [4]
CHARACTERIZATION.
RP MEDLINE=96205869; PubMed=8635464;
RX Zhao J.J., Lazzarini R.A., Pick L.;
RA "Functional dissection of the mouse Hox-a5 gene.";
RL EMBO J. 15:1313-1322(1996).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC 5'-CYNNATTA[TC]Y-3'.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
CC KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M36604; AAA37838.1; -.
DR EMBL: Y00208; CAA68364.1; -.
DR EMBL: X16840; CAA34738.1; -.
DR EMBL: M28021; AAA37837.1; -.
DR PIR: S07812; WJMS13.
DR HSP: P02833; ISAN.
DR TRANSFAC: T00377; -.
DR MGI: MGI:96177; Hoxa5.
DR InterPro: IPR001356; -.
DR InterPro: IPR001827; -.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00025; ANTENNAPEDIA.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 176 181 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 195 254 HOMEBOX.
FT SEQUENCE 270 AA; 29237 MW; DC4BDDA8FE62766E CRC64;

Query Match 9.5%; Score 86; DB 1; Length 270;
Best Local Similarity 25.8%; Pred. No. 4.6;
Matches 55; Conservative 13; Mismatches 63; Indels 82; Gaps 11;
QY 10 SEQ-EDSSAERG-----LGPSPAGDPSGSGKHHRQ-----APGLWDASHQ 51
DB 31 SEQFRDSASMHSGRYGYNGMDLSVGRSGSGHFGSGERARSYAAGASAP-----AEPR 85
QY 52 QEQTSS-----SHHG-----AGAVEIRSR-----72
DB 86 YSQPATSTHPPDPPLPCSAVAPSPGSDSHHGKNSLGNSSGASANAGSTHSSREGVGT 145
QY 73 ----HSSYPAGTDEDEGMGEPSFPRGRSRAPPNLAQAQRYGRELRRMSDEFVDFSKG 128

CC -!- PTM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT
CC PROTEIN KINASE (CGPK) IN PLATELETS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z46389; CAA86523.1; -
DR EMBL; X98534; CAA67147.2; -
DR EMBL; X98533; CAA67147.2; JOINED.
DR MIM; 601703; -
DR InterPro: IPR001960; -
DR Pfam: PF00568; WHI; 1; -
KW Phosphorylation; Actin-binding.
FT DOMAIN 118 122 POLY-PRO.
FT DOMAIN 170 186 POLY-PRO.
FT DOMAIN 215 222 POLY-GLY.
FT DOMAIN 259 262 POLY-GLY.
FT DOMAIN 322 325 POLY-SER.
FT MOD_RES 137 157 PHOSPHORYLATION (BY CAPK AND CGPK).
FT MOD_RES 239 239 PHOSPHORYLATION (BY CAPK AND CGPK).
FT MOD_RES 278 278 PHOSPHORYLATION (BY CAPK AND CGPK).
SQ SEQUENCE 380 AA; 39830 MW; 17634B8134DEBF59 CRC64;

Query Match 9.4%; Score 85; DB 1; Length 380;
Best Local Similarity 24.9%; Pred. No. 7.8;
Matches 43; Conservative 18; Mismatches 52; Indels 60; Gaps 10;
QY 17 SAERGLG-----PSPAGDGPSSGKHHRQAPGL-----LWDASHQEQE---PTS- 57
DB 195 AAHAGAGGPPPPAPPLPAAGPGGG---AGAPGLAAATAGAKLRVKQEAEGCGTAP 251
QY 58 ---SSHHGGAGAVE-----IRSRHSSYPAG---TEDEGMGEEPS-----PPR 94
DB 252 KAESGRSGGGLMEENAMLARRKATQVGEKTPKDSANQAEPEARVPAQSESVRPWE 311
QY 95 GRSRAP-----PMLAAQRYGRELREMSDEFVDSFKKGLPRK 133
DB 312 KNSTTLPRMKSSSVTTSETQCTPSSSDYS-DLQRVKQELLEVEVKELQVKR 363

RESULT 15
ID Y553_HUMAN STANDARD; PRT; 1089 AA.
AC Q9UKJ3; O60300;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN KIAA0553.
GN KIAA0553.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res..5:31-39(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99408744; PubMed=10477733;
RA Thornton M.A., Poncz M., Korostishevsky M., Yakobson E., Usher S.,

RA Seligsohn U., Peretz H.;
RT "The human platelet alphaIIb gene is not closely linked to its
RT integrin partner beta3.";
RL Blood 94:2039-2047(1999).
CC
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CC
CC EMBL; AB011125; BAA25479.1; ALT_INIT.
DR EMBL; AF160252; AAF03681.1; -
KW Hypothetical protein.
FT DOMAIN 263 266 POLY-LYS.
FT DOMAIN 332 336 POLY-ARG.
FT DOMAIN 359 362 POLY-GLY.
FT DOMAIN 425 430 POLY-GLU.
FT DOMAIN 456 461 POLY-SER.
FT DOMAIN 971 977 POLY-ALA.
FT DOMAIN 1059 1065 POLY-ALA.
FT CONFLICT 207 207 K -> E (IN REF. 1).
FT CONFLICT 267 267 E -> K (IN REF. 1).
FT CONFLICT 278 278 P -> H (IN REF. 1).
FT CONFLICT 846 846 G -> S (IN REF. 1).
SQ SEQUENCE 1089 AA; 117999 MW; 4EF687F9D81A16A5 CRC64;

Query Match 9.4%; Score 85; DB 1; Length 1089;
Best Local Similarity 19.9%; Pred. No. 23;
Matches 58; Conservative 22; Mismatches 71; Indels 140; Gaps 11;
QY 12 QEDSSA---ERGLPSPAGDGPSSGKHHRQAPGLWDASHQEQE--- 55
DB 304 KKNKSAPADSEKGPKEPPGSGSPAPRRRAQ---DSSQRLPAEESSGKKDEG 359
QY 56 ---TSSSHRG---AGAV-EIRSRHSSYPAG--- 79
DB 360 GGGSSQDHGGRKHGKELPPSCQRRAGTKRSRSHRSQPSGDESDSDASSHRLHQS 419
QY 80 ---TEDEGMGEEPSFGRS---RSAPPLWAAQR--- 109
DB 420 PSQYEEEEEDSGSEHSRGRSRGRHSHRSRYSSSSDASSDQSCYSRQRSYSD 479
QY 110 ---YGRELRMSDFVD--- 123
DB 480 SYSDYSDRSRRHSHSDSDDYASSKRSRKHYSDDDDYSLSCSRSRSHRTRE 539
QY 124 -SFKKGLPRKSAQTATMRQSSSWTRVFSW---WDRNLGRGSSAFSQ 168
DB 540 RSRGRSRSSSCSRSRKRRSRSTTA--HSQWRSRYSRDRSRSTRSPSQ 588

Search completed: October 9, 2001, 15:55:20
Job time: 195 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:51:45 ; Search time 46.39 Seconds
(without alignments)
479.139 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIPEFEPSEQEDSSSAER.....RVFQSWDRNLGRSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phase:*
10: sp-plant:*
11: sp-rodent:*
12: sp-unclassified:*
13: sp-vertebrate:*
14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	905	100.0	168	014803	014803 homo sapien
2	636.5	70.3	205	11	035147
3	636.5	70.3	205	11	070256
4	446	49.3	220	11	09JHX1
5	207.5	22.9	95	13	09I9N2
6	100	11.0	608	14	09QSK9
7	98.5	10.9	569	13	09DF20
8	98	10.8	272	4	09NS37
9	98	10.8	355	2	09RDL8
10	97.5	10.8	867	10	09FV26
11	97	10.7	1146	5	09N8Q9
12	96.5	10.7	980	4	09S387
13	96.5	10.7	2506	4	09NS88
14	95.5	10.6	923	5	09NKN4
15	95	10.5	622	4	09NTE2
16	95	10.5	701	4	09NTP8
17	95	10.5	803	4	09ULK9
18	94	10.4	474	5	09VA96
19	93.5	10.3	549	4	09H0B9

20	93.5	10.3	1203	4	Q9UPQ9	Q9upq9 homo sapien
21	93.5	10.3	1729	5	Q25734	Q25734 plasmodium
22	93	10.3	1300	14	Q36421	Q36421 alcelaphine
23	93	10.3	2472	4	Q9NS89	Q9ns89 homo sapien
24	92.5	10.2	336	14	Q98321	Q98321 molluscum c
25	92.5	10.2	1082	11	Q9EP02	Q9epu2 rattus norv
26	92.5	10.2	1398	11	Q09000	Q09000 mus musculu
27	92	10.2	670	5	Q9NEL2	Q9nel2 caenorhabdi
28	91.5	10.1	651	4	Q9NXI9	Q9pxi9 homo sapien
29	91.5	10.1	845	4	Q9HAU3	Q9hau3 homo sapien
30	91.5	10.1	990	4	Q15206	Q15206 homo sapien
31	91.5	10.1	1218	4	Q05331	Q05331 homo sapien
32	90.5	10.0	662	5	Q9VW76	Q9vw76 drosophila
33	90.5	10.0	947	10	Q9LWJ9	Q9lwi9 oryza sativ
34	90	9.9	476	10	Q9FFH8	Q9ffh8 arabidopsis
35	90	9.9	903	4	Q9UPX1	Q9upx1 homo sapien
36	89.5	9.9	845	4	Q9HBB5	Q9hbb5 macropros ru
37	89	9.8	410	6	Q97645	Q97645 mus musculu
38	89	9.8	414	11	Q9ER08	Q9eru8 mus musculu
39	89	9.8	462	6	Q97643	Q97643 lama glama
40	89	9.8	735	11	Q9JIG4	Q9jiq4 mus musculu
41	88.5	9.8	393	11	Q08719	Q08719 rattus norv
42	88.5	9.8	393	11	P70429	P70429 mus musculu
43	88.5	9.8	510	5	Q9VAI8	Q9vai8 drosophila
44	88.5	9.8	658	11	Q9JL61	Q9jl61 mus musculu
45	88.5	9.8	667	14	Q9PY84	Q9py84 rat cytomeg

ALIGNMENTS

RESULT 1
014803 PRELIMINARY; PRT; 168 AA.
AC 014803;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).
GN BAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97083574; PubMed=8929532;
RA Wang H.G., Rapp U.R., Reed J.C.;
RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
RL Cell 87:629-638(1996).
RN [2]
RP SEQUENCE FROM N.A.
RL Takayama S., Reed J.C.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ottillie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,
RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;
RL J. Biol. Chem. 0:0-0(1997).
DR EMBL; AF021792; AAB72092.1; -.
DR EMBL; AF031523; AAB88124.1; -.
FT NON_TER 1
SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 100.0%; Score 905; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFEPSEQEDSSSAERGLGPSAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60
|||||
Db 1 MFQIPEFEPSEQEDSSSAERGLGPSAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60

```
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSDE 120
|||||
DB 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSDE 120
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||
DB 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||

RESULT 2
O35147
ID O35147 PRELIMINARY; PRT; 205 AA.
AC O35147;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER.
DE BCL-2 ASSOCIATED DEATH PROMOTER.
GN BAD.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
DR EMBL; AF003523; AAC53374.1; -.
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;

Query Match 70.3%; Score 636.5; DB 11; Length 205;
Best Local Similarity 75.1%; Pred. No. 3.1e-51;
Matches 127; Conservative 11; Mismatches 24; Indels 7; Gaps 4;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
DB 43 MFOIPEFEPSEQEDASTDRGLGSLTDEQP---GPY--LAPGLLSIVQQPGQAANN 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSD 119
|||||
DB 98 HGGAGTMTETRSRHSYPAGTDEDEGMGEELSPFRGRSRAPPNLWAAQRYGRELRMSD 157
|||||

QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||
DB 158 EFEGSP-KGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSGSTPSQ 205
|||||

RESULT 4
Q9JHX1
ID Q9JHX1 PRELIMINARY; PRT; 220 AA.
AC Q9JHX1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.
GN BAD-BETA.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamer S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279911; AAF91428.1; -.
SQ SEQUENCE 220 AA; 24278 MW; E27BCD7C969E90F CRC64;

Query Match 49.3%; Score 446; DB 11; Length 220;
Best Local Similarity 72.4%; Pred. No. 1.2e-33;
Matches 92; Conservative 8; Mismatches 21; Indels 6; Gaps 3;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
DB 43 MFOIPEFEPSEQEDASTDRGLGSLTDEQP---GPY--LAPGLLSIVQQPGQAANN 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSD 119
|||||
DB 98 HGGAGTMTETRSRHSYPAGTDEDEGMGEELSPFRGRSRAPPNLWAAQRYGRELRMSD 157
|||||

QY 120 EFVDSFK 126
DB 158 EFEGSPK 164
|||||

RESULT 5
Q9I9N2
ID Q9I9N2 PRELIMINARY; PRT; 95 AA.
AC Q9I9N2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
```



```

Db 194 GLARLLSLSGVGLRLTSLFR 215
      || | | : : | : | |
      || | | : : | : | |

RESULT 9
Q9RDL8 PRELIMINARY; PRT; 355 AA.
AC Q9RDL8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE DNA-BINDING PROTEIN.
GN SC123.06C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Brown S.P., Harris D.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RA "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL136518; CAB66246.1; -
DR InterPro; IPR000445; -
DR SMART; PF00633; HHH; 1.
DR SMART; SM00278; HHH1; 1.
KW DNA-binding.
SQ SEQUENCE 355 AA; 36853 MW; ELE9D0A574CCABDE CRC64;

Query Match 10.8%; Score 98; DB 2; Length 355;
Best Local Similarity 28.5%; Pred. No. 0.2;
Matches 43; Conservative 14; Mismatches 66; Indels 28; Gaps 7;

QY 15 SSSAERGLGSPAGDGPSSGKHKHQAPGLLDASHQEQPTSSHHG--GAGAVEIRSR 72
      :|| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      :|| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 TASATSGPRAPASDGLA----HRRAPGSRTHARH-----SHARHGRHRAAPEELRR 59

QY 73 -HSSYPAGTDEDEGMEEPFRRSRAP--PNLWAAQRYGRELRRMSDEFVDSFKGL 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 AETFAERAGYDHAGHEGA--HGCTKGGLPLGLDAPARQGSPL-----PGL 105

QY 130 PRPKSAGTATQMRQSSSWTRVFQSWMDNLG 160
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 106 DATPGTAWRERAGSALRRMPLNLQTRCG 136

RESULT 10
Q9FVZ6 PRELIMINARY; PRT; 867 AA.
AC Q9FVZ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE REPLICATION PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
```

```

OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Hsiao J., Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNB0073N24 genomic sequence.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC078840; AAG13631.1; -
SQ SEQUENCE 867 AA; 94083 MW; 4FEA69E1BFC0CB2C CRC64;

Query Match 10.8%; Score 97.5; DB 10; Length 867;
Best Local Similarity 28.0%; Pred. No. 0.55;
Matches 37; Conservative 10; Mismatches 46; Indels 39; Gaps 5;

QY 13 EDSSSAERGLGSPAG----DGPSGSGKHKHQAP-----GLLDASHQEQE--- 53
      : : : | | | | | | | | | | | | | | | | | | | | | | |
      : : : | | | | | | | | | | | | | | | | | | | | | | |
Db 730 KEFAAAARGGPDPLSHSLGGGGTGKEAAAPPTRGASRGGGGADAGSEQEDAA 789

QY 54 -----OPTSSSHHGAGAVEIRSRHSSYPAGTDEDEGMEEPFRRSRAPPNLWAA 107
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 790 AWGGGPDPLSHSLGGGG-----GTGKEEA-AAAPTPTRGASRGGGGGGTGT 835

QY 108 QRYGRELRRMSD 119
      : | | | | | :
      : | | | | | :
Db 836 RREERLRREE 847

RESULT 11
Q9N8Q9 PRELIMINARY; PRT; 1146 AA.
AC Q9N8Q9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE POSSIBLE CALPAIN-LIKE PROTEASE.
GN CH1.189.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TREU927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359782; CAB95474.1; -
DR InterPro; IPR001300; -
DR Pfam; PF00648; Peptidase_C2; 1.
DR PRINTS; PR00704; CALPAIN.
DR SMART; SM00230; CysPC; 1.
KW Protease.
SQ SEQUENCE 1146 AA; 126154 MW; 89FC36E433768B8F CRC64;

Query Match 10.7%; Score 97; DB 5; Length 1146;
Best Local Similarity 23.2%; Pred. No. 0.82;
Matches 46; Conservative 18; Mismatches 90; Indels 44; Gaps 7;

QY 6 EPEPSQEDSSSAERGLGSPAG-----DGPSSGKHKHQAPGLLDAS 49
      | | | | : | | | | | | | | | | | | | | | | | | | | | |
      | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db 80 ESEAKESDGRAEEASPAPSPAGESDEKASKSEHSEVKEGSDGRAEEASPAPS---PAG 136

QY 50 HQEQPTSSSH-----HGGAGAVEIRSRHSSYPAGTDEDD-----EGMEE 89
      : : : | | | | | | | | | | | | | | | | | | | | | | |
      : : : | | | | | | | | | | | | | | | | | | | | | | |
Db 137 ESEKASKSEHSEVKEGSDGRAEEASPAPS-PAGESDEKASKSEHSEVKEGSDGRAEE 195

QY 90 PSPFRRSRAPPNLWAAQRYGRELRRMSDEFVDSFKGLPRPKSAGTATQMRQSSSWTR 149
```

RESULT	13	
Q9NS88		
ID	Q9NS88	PRELIMINARY; PRT; 2506 AA.
AC	Q9NS88;	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE	ALPHA-VOLTAGE-DEPENDENT CALCIUM CHANNEL.	
GN	CACNA1A.	
GN	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata;	Cranialta; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates;	Catarrhini; Hominoidea; Homo.

```
Query Match      10.6%; Score 95.5; DB 5; Length 923;
Best Local Similarity 26.4%; Pred. No. 0.9;
Matches 33; Conservative 21; Mismatches 44; Indels 27; Gaps 7;

QY 10 SEQEDSSSAERGLGPSAGDGPSSGKRRHROAPGILLMDASHQQEPTSSSHHGAGAVEI 69
    :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :
```

Db 802 AEQRTNTDDR-----SPSAGGPASADVHRSA-----SQPQPHS-----HAGGSAL-V 845
QY 70 RSRHSYPAGTEDEGMGEPPSPFGR--SRSPNLMWAAQRYGRELRRMSDEFVDSFKK 127
Db 846 SNHNGVQAAA-----SGTGRMSAANSRGNVGVPP-----RNGRRRAPLAAILDTLTA 896
QY 128 GLPRP 132
Db 897 GPPQP 901

RESULT 15

Q9NTE2
ID Q9NTE2 PRELIMINARY; PRT; 622 AA.
AC Q9NTE2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE HYPOTHETICAL 67.3 KDA PROTEIN (FRAGMENT).
GN DKFZP434B239.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI37336; CAB70699.1; -
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 622 AA; 67337 MW; 11D6CDF0E2D06082 CRC64;

Query Match 10.5%; Score 95; DB 4; Length 622;
Best Local Similarity 27.6%; Pred. No. 0.67;
Matches 50; Conservative 17; Mismatches 50; Indels 64; Gaps 11;
QY 13 EDSSSAERGLGSPSP--AGDPSGSGKHHRQAPGLLWDASHQEQPTSSSHHGAGAVEI 69
Db 14 EEKKHAEAPAGENPPRPGDARAGSK-----AKPQESPSSAS--ALAEWASI 60
QY 70 RSR-----HSSYPAGTEDDE-GMGEPPSP-----FRGRSRAPP-----NLWAAQRY---- 110
Db 61 RSRILKNAESDPRSSERDQLRPGDESTPRGCDSDRGNRKTPPVNAKFSIMPWQKFSDG 120
QY 111 GRELRMSDEFVDSFKK-----GLPRPKSAGTATOMRQSSSWTRVFQSWWDRNLGR 161
Db 121 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPAGV-----RELGK 160
QY 162 G 162
Db 161 G 161

Search completed: October 9, 2001, 15:54:56
Job time: 191 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:50:04 ; Search time 44.37 Seconds
(without alignments)
229.543 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIEFEPSEQEDSSAER.....RVFSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
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5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.*
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19: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	905	100.0	168	19	AAW55779 Human Bcl-xL/Bcl-2
2	905	100.0	168	21	AA13512 Human cell prolif
3	905	100.0	168	22	AA13512 Human BAD mutant a
4	905	100.0	168	22	AA13512 Human BAD mutant a
5	751	83.0	166	18	AAW32476 BCC6 protein for r
6	649	71.7	162	22	AA1994 Shorter murine BAD
7	649	71.7	204	17	AA195168 bcl-x(L)/bcl-2 ass
8	649	71.7	204	19	AAW61315 Murine BCL-XL/BCL-
9	649	71.7	204	19	AAW58832 Murine BAD protein
10	649	71.7	204	22	AA1994 Longer murine BAD
11	646	71.4	204	19	AAW61317 Mutant BCL-XL/BCL-

12	643	71.0	204	19	AAW61316 Mutant BCL-XL/BCL-
13	643	71.0	204	19	AAW61318 Mutant BCL-XL/BCL-
14	314	34.7	59	19	AAW61319 Mutant BCL-XL/BCL-
15	314	34.7	59	19	AAW61320 Mutant BCL-XL/BCL-
16	311	34.4	59	19	AAW61321 Mutant BCL-XL/BCL-
17	308	34.0	59	19	AAW61322 Mutant BCL-XL/BCL-
18	159	17.6	56	21	AAW61323 Human secreted pro
19	133	14.7	26	21	AAW61324 Mammalian Bad Bcl-
20	133	14.7	26	22	AAW61325 BAD BH3 consensus
21	120.5	13.3	27	21	AAW61326 Bcl2 polypeptide B
22	116	12.8	23	17	AAW61327 bcl-x(L)/bcl-2 ass
23	114	12.6	26	21	AAW61328 Bcl2 polypeptide B
24	114	12.6	26	21	AAW61329 Bcl2 polypeptide B
25	114	12.6	27	21	AAW61330 Bcl2 polypeptide B
26	114	12.6	28	21	AAW61331 Human neuronal cal
27	97	10.7	2510	16	AAW61332 Human calcium chan
28	97	10.7	2510	21	AAW61333 Human SCA6 protein
29	96.5	10.7	1182	20	AAW61334 Human calcium chan
30	94	10.4	1931	13	AAW61335 Human cytoskeleton
31	93.5	10.3	395	21	AAW61336 A human proliferat
32	93.5	10.3	549	21	AAW61337 Truncated Plasmodi
33	93.5	10.3	1726	17	AAW61338 Murine PCIP protei
34	92.5	10.2	1447	20	AAW61339 Arabidopsis thalia
35	90	9.9	397	21	AAW61340 Arabidopsis thalia
36	90	9.9	420	21	AAW61341 Peptide fragment o
37	90	9.9	434	17	AAW61342 Human N-type calci
38	90	9.9	434	21	AAW61343 Arabidopsis thalia
39	90	9.9	476	21	AAW61344 Human neuronal cal
40	90	9.9	2237	16	AAW61345 Human calcium chan
41	90	9.9	2237	19	AAW61346 Human calcium chan
42	90	9.9	2237	21	AAW61347 Human calcium chan
43	90	9.9	2337	19	AAW61348 Sequence of the al
44	90	9.9	2339	14	AAW61349 Human neuronal cal
45	90	9.9	2339	16	AAW61350

ALIGNMENTS

RESULT 1

AAW55779 AAW55779 standard; Protein; 168 AA.

XX AC AAW55779;

XX DT 17-JUL-1998 (first entry)

XX DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;

XX KW programmed cell death; apoptosis.

XX OS Homo sapiens.

XX PN WO9812328-A2.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-US16991.

XX PR 20-SEP-1996; 96US-0717123.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Horne WA, Oltersdorf T;

XX DR WPI; 1998-217267/19.

XX DR N-PSDB; AAV25877.

XX PT Bad gene mediating apoptosis - used to develop products for treating

XX PT e.g. neurodegenerative disease, cancers or autoimmune disease

XX PS Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated
CC death promoting polypeptide, Bad, the binding of which to Bcl-XL
CC results in the induction of programmed cell death, i.e. apoptosis.
CC Bad can be used in screening assays for compounds to treat or
CC prevent diseases characterised by apoptotic cell death, such as
CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
CC aplastic anaemia and ischaemic injury including myocardial
CC infarction, stroke and reperfusion injury. Assays can also be
CC used to obtain apoptosis enhancing compounds to treat or prevent
CC diseases characterised by the loss of apoptotic cell death, such as
CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
CC diseases, e.g. systemic lupus erythematosus and immune-mediated
CC glomerulonephritis and viral infections, e.g. herpesvirus,
CC poxvirus or adenovirus infection. Bad can also be used for
CC detection and diagnosis.
XX
SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 19; Length 168;
Best Local Similarity 100.0%; Pred. No. 6.4e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLDASHQOEPTSSSH 60
DB 1 mqiipfefseqedssaaerglgpspagdgpsgghkhrqapglldashqoeptsssh 60
QY 61 HGAGAVEIRSHSSYPAGTEDDEGMGEFPSPFRGRSRAPPNLMAAQRYGRELRRMSDE 120
DB 61 hgagaveirshssypagteddegmggeepsfgrgrsappnlwaaqrygrellrmsde 120
QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWDRLNLRGSSAPSQ 168
DB 121 fvdskkglprpksagtatqmrqssswtrvfqswdrlnlgssapsq 168

RESULT 2
AAB13512
ID AAB13512 standard; protein; 168 AA.
XX
AC AAB13512;
XX
DT 02-NOV-2000 (first entry)
XX
DE Human cell proliferation protein APOP-1.
XX
KW Human; cell proliferation; APOP-1; cancer; inflammation; infection;
KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.
XX
OS Homo sapiens.
XX
PN US6080847-A.
XX
PD 27-JUN-2000.
XX
PF 04-DEC-1997; 97US-0985335.
XX
PR 04-DEC-1997; 97US-0985335.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Corley NC, Hillman JL, Yue H, Lal P, Shah P;
XX
DR WPI; 2000-451230/39.
DR N-PSDB; AAA63332.
XX
PT Novel polynucleotide and polypeptide sequences of proteins associated
PT with cell proliferation for diagnosis, prevention and treatment of e.g.
PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease -

PS Example 8; Fig 1; 58pp; English.
XX
XX The present sequence is the human APOP-1 protein. This protein, which
CC shares structural and chemical homology with Bcl-2, is involved in cell
CC proliferation. Its coding sequence was isolated by screening a synovial
CC tissue cDNA library using a computer search for amino acid sequence
CC alignments. The gene and protein can be used in the treatment of various
CC cancers, disorders with associated inflammation such as Addison's
CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
CC of cancer, haemodialysis and extracorporeal circulation, infections,
CC trauma, disorders with associated apoptosis including AIDS and other
CC infectious and genetic immunodeficiencies, neurodegenerative diseases
CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
CC such as myocardial infarction, and wasting diseases including cachexia.
XX
SQ Sequence 168 AA;

Query Match 100.0%; Score 905; DB 21; Length 168;
Best Local Similarity 100.0%; Pred. No. 6.4e-88;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLDASHQOEPTSSSH 60
DB 1 mqiipfefseqedssaaerglgpspagdgpsgghkhrqapglldashqoeptsssh 60
QY 61 HGAGAVEIRSHSSYPAGTEDDEGMGEFPSPFRGRSRAPPNLMAAQRYGRELRRMSDE 120
DB 61 hgagaveirshssypagteddegmggeepsfgrgrsappnlwaaqrygrellrmsde 120
QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWDRLNLRGSSAPSQ 168
DB 121 fvdskkglprpksagtatqmrqssswtrvfqswdrlnlgssapsq 168

RESULT 3
AAB70368
ID AAB70368 standard; protein; 168 AA.
XX
AC AAB70368;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human BAD mutant amino acid sequence SEQ ID NO:1.
XX
KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnary;
KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
KW immunodeficiency disease; neurodegenerative disease; viral infection;
KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
KW lymphoproliferative condition; inflammation; autoimmune disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200110888-A1.
XX
PD 15-FEB-2001.
XX
PF 30-MAY-2000; 2000WO-US11864.
XX
PR 28-MAY-1999; 99US-0136783.
XX
PA (APOP-) APOPTOSIS TECHNOLOGY INC.
XX
PI Zhou X;

DR WPI; 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -

XX Claim 1; Page 147; 157pp; English.

XX The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC nootropic, antiischaemic, vulnerary, cytostatic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed human BAD mutant amino acid sequence from the present invention.

XX Sequence 168 AA;

Query Match 100.0%; Score 905; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. No. 6.4e-88;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60
 Db 1 mfpifepseqedsssaerglgspagdgpsgskhhrqapglldashhgqeqptsssh 60

Qy 61 HGGAGAVEIRSHSSYPAGTDEGMEEPSPFGRGRSRAPPNLWAAQRYGRELRRMSDE 120
 Db 61 hggagaveirshssypagtdedgmgeepsfgrgrsrappnlwaaqrygrellrmsde 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
 Db 121 fvdskkglprpksgatqmrqssswtrvfqswmdrnlgrgssapsq 168

RESULT 4

AAB48287

ID AAB48287 standard; protein; 168 AA.

XX AAB48287;

XX 02-APR-2001 (first entry)

XX Human Bad protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic.

XX Homo sapiens.

XX WO200075184-A1.

XX 14-DEC-2000.

XX 05-JUN-2000; 2000WO-US15449.

XX 04-JUN-1999; 99US-0137494.

XX (UYVA) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;
 XX WPI; 2001-061703/07.
 DR N-FSDB; AAC84599.

XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -

XX Claim 5; Page 102-103; 162pp; English.

XX The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.

XX Sequence 168 AA;

Query Match 100.0%; Score 905; DB 22; Length 168;
 Best Local Similarity 100.0%; Pred. No. 6.4e-88;
 Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60
 Db 1 mfpifepseqedsssaerglgspagdgpsgskhhrqapglldashhgqeqptsssh 60

Qy 61 HGGAGAVEIRSHSSYPAGTDEGMEEPSPFGRGRSRAPPNLWAAQRYGRELRRMSDE 120
 Db 61 hggagaveirshssypagtdedgmgeepsfgrgrsrappnlwaaqrygrellrmsde 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
 Db 121 fvdskkglprpksgatqmrqssswtrvfqswmdrnlgrgssapsq 168

RESULT 5

AAW32476

ID AAW32476 standard; Protein; 166 AA.

XX AAW32476;

XX 15-JAN-1998 (first entry)

XX BBC6 protein for regulating cell death.

XX BBC6 gene; cell death; cell cycle; Bcl2; human.

XX Homo sapiens.

XX US5663316-A.

XX 02-SEP-1997.

XX 18-JUN-1996; 96US-0665617.

XX 18-JUN-1996; 96US-0665617.

XX (CLON-) CLONTECH LAB INC.

XX Xudong Y;

XX WPI; 1997-447980/41.

DR N-FSDB; AAT91561.

XX Isolated BBC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2

XX PS Claim 1; Column 11-12; 7pp; English.

CC The present sequence represents a protein of 166 amino acids. The

CC sequence is disclosed as being a protein called Bcl-2 which regulates

CC cell death through interaction with Bcl-2. The DNA may be used for the

CC production of the recombinant protein, which can be used in unspecified

CC therapeutic or diagnostic procedures, as a molecular weight marker, and

CC to raise antibodies that can be used in unspecified diagnostic or

CC therapeutic applications and to reduce or eliminate the biological

CC activity of the Bcl-2 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 83.0%; Score 751; DB 18; Length 166;

Best Local Similarity 84.0%; Pred. No. 1.2e-71;

Matches 147; Conservative 3; Mismatches 9; Indels 16; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDPSGSGKHHKQAPG-----LLWDASHQOE 53

DB 1 mfgipefepsegedsssaerg-wrspagtq-----qapasiiarpqyldashqae 51

QY 54 QPTSSHHGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRGAPPNLWAAQRYGRE 113

DB 52 qptssshhgagaveirsrhssypagteddegmggeepsfgrgararppppnlwaaqrygre 111

QY 114 LRRMSDEFVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 112 lrrmsdefvdsfkkgprpksagtatqmrqssswtrvfqswmdrnlgrgtaapsq 166

RESULT 6

AAB70370

ID AAB70370 standard; protein; 162 AA.

XX AC AAB70370;

XX DT 02-MAY-2001 (first entry)

XX DT Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

XX KW immunostimulant; neuroprotective; nontropic; antiischaemic; vulnary;

XX KW cytostatic; antiviral; antithratic; antiinflammatory; wound healing;

XX KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

XX KW immunodeficiency disease; neurodegenerative disease; viral infection;

XX KW ischaemic cell death; reperfusion cell death; arthritis; infertility;

XX KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.

XX OS Synthetic.

XX XX WO200110888-A1.

XX PN 15-FEB-2001.

XX PD 30-MAY-2000; 2000WO-US11864.

XX PF 28-MAY-1999; 99US-0136783.

XX PR (APOB-) APOPTOSIS TECHNOLOGY INC.

XX PA Zhou X;

XX PI WPI; 2001-138734/14.

XX DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,

XX PT useful for screening for candidate compounds which induce or inhibit

XX PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or

XX PT Ser113 -

XX PS Claim 7; Page 148-149; 157pp; English.

XX CC The present invention describes an isolated or synthetic polypeptide

CC (I) comprising a less than full length amino acid sequence of a mutant

CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

CC fragment, which contains amino acid substitutions at Ser118 of a human

CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,

CC nontropic, antiischaemic, vulnary, cytostatic, antiviral,

CC antithratic, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC identified and (mutant) BAD polypeptides are useful in treating

CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

CC death, reperfusion cell death, wound healing, cancer, viral infections,

CC lymphoproliferative conditions, arthritis, infertility, inflammation and

CC autoimmune diseases. The present sequence represents a specifically

CC claimed shorter murine BAD mutant amino acid sequence from the present

CC invention.

XX SQ Sequence 162 AA;

Query Match 71.7%; Score 649; DB 22; Length 162;

Best Local Similarity 75.6%; Pred. No. 6.7e-61;

Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDPSGSGKHHKQAPG-----LLWDASHQOEPTSSSH 60

DB 1 mfgipefepsegedsssaerg-wrspagtq-----qapasiiarpqyldashqae 55

QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRGAPPNLWAAQRYGRELRMSDE 120

DB 56 hgagaveirsrhssypagteddegmggeepsfgrgararppppnlwaaqrygrelrmsde 115

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 116 fegsf-kglprpksagtatqmrqsgwttriigswdrlngkggstpsq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AC AAR95168;

XX XX 06-JAN-1997 (first entry)

XX DE bcl-x(L)/bcl-2 associated death promoter protein.

XX KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

XX KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;

XX KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

XX KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX OS Mus musculus.

XX FH Location/Qualifiers

XX FT 147..149

XX FT /note= "BH1 conserved amino acids"

XX FT 191..192

XX FT /note= "BH2 conserved amino acids"

XX FT 38..61

XX FT /note= "PEST sequence"

XX FT 111..130

XX FT /note= "PEST sequence"

XX XX WO9613614-A1.

XX PN 09-MAY-1996.

XX PD 31-OCT-1995; 95WO-US14246.

```
XX PR 31-OCT-1994; 94US-03333565.
XX XX (UNIW ) UNIV WASHINGTON.
XX XX Korsmeyer SJ;
XX XX WPI; 1996-251465/25.
XX DR N-PSDB; AAT29479.
XX XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
XX PT useful to treat neoplasia and apoptosis and to identify agents
XX PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
XX XX
XX PS Claim 3; Fig 1; 130pp; English.
XX XX
XX CC This sequence represents the murine bcl-x(L)/bcl-2 associated death
XX CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
XX CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
XX CC to the bcl-2-related family clustered in the BHL and BH2 domain. Bad
XX CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
XX CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
XX CC death inhibitory activity of bcl-x(L), but is much less effective at
XX CC countering the death inhibitory activity of bcl-2. Bad expression can
XX CC accelerate apoptotic cell death induced by cytokine deprivation in an
XX CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the
XX CC death repressor activity of bcl-x(L). Bad competes with Bax for binding
XX CC to bcl-x(L). Bad may be used to identify agents which inhibit its
XX CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
XX CC used to treat neurodegenerative diseases, immunodeficiency diseases,
XX CC e.g. AIDS, senescence or ischaemia.
XX XX
XX SQ Sequence 204 AA;

Query Match 71.7%; Score 649; DB 17; Length 204;
Best Local Similarity 75.6%; Pred. No. 9.1e-61;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPSPQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
DB 43 mfiqipefepseqedasatdrglpsltedqp---gpy--lapgllgsnihqggraatnsh 97

QY 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFRGRSRSPPNLWAAQRYGRELRMSDE 120
DB 98 hggagametrshssypagteedegmeelspfgrsrsappnlwaaqrygrelrmsde 157

QY 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
DB 158 fegsf-kglprksagatqmrqsagwtrliqswwdrnlgkggstpsq 204

RESULT 8
AAW61315
ID AAW61315 standard; Protein; 204 AA.
XX XX
XX AC AAW61315;
XX XX
XX DT 07-OCT-1998 (first entry)
XX XX
XX DE Murine BCL-XL/BCL-2 associated cell death regulator.
XX XX
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX KW serine substituted mutant; apoptosis; cancer; viral infection.
XX XX
XX OS Mus sp.
XX XX
XX PN WO9817682-A1.
XX XX
XX PD 30-APR-1998.
XX XX
XX PF 17-OCT-1997; 97WO-US19175.
XX XX

PR 18-OCT-1996; 96US-07333505.
XX XX (UNIW ) UNIV WASHINGTON.
XX XX Korsmeyer SJ;
XX XX WPI; 1998-261422/23.
XX DR N-PSDB; AAV27833.
XX XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX PT useful for, e.g. treating reduced apoptosis such as in cancer or
XX PT viral infection
XX XX
XX PS Claim 1; Fig 10; 95pp; English.
XX XX
XX CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX CC death regulator) proteins, having an amino acid other than Ser at
XX CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX CC present sequence is the murine BAD protein. Also described are: (1)
XX CC fragments of mutant BAD protein able to decrease cell viability; (2)
XX CC fusion proteins of mutant BAD with a heterologous polypeptide that
XX CC increases intracellular delivery. Mutant BAD proteins are used to treat
XX CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX CC viral infection, lymphoproliferation, arthritis, infertility,
XX CC inflammation and autoimmune disease. Polynucleotide sequences encoding
XX CC mutant BAD proteins can be used similarly by gene therapy or to produce
XX CC transgenic animals for use as disease models or in drug screening. BAD
XX CC proteins phosphorylated at specified Ser are used to screen for enhancers
XX CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX CC aging or ischaemic cell death. The apoptotic status of cells is
XX CC determined by measuring relative amounts of phosphorylated and non-
XX CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX CC greater death-promoting activity than wild-type BAD which can become
XX CC phosphorylated on the specified Ser, forming a product that does not
XX CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX CC proteins in the cytosol, thus promoting cell survival. The mutants with
XX CC Ser substituted cannot bind 14-3-3.
XX XX
XX SQ Sequence 204 AA;

Query Match 71.7%; Score 649; DB 19; Length 204;
Best Local Similarity 75.6%; Pred. No. 9.1e-61;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPSPQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
DB 43 mfiqipefepseqedasatdrglpsltedqp---gpy--lapgllgsnihqggraatnsh 97

QY 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPFRGRSRSPPNLWAAQRYGRELRMSDE 120
DB 98 hggagametrshssypagteedegmeelspfgrsrsappnlwaaqrygrelrmsde 157

QY 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
DB 158 fegsf-kglprksagatqmrqsagwtrliqswwdrnlgkggstpsq 204

RESULT 9
AAW58832
ID AAW58832 standard; protein; 204 AA.
XX XX
XX AC AAW58832;
XX XX
XX DT 23-JUL-1998 (first entry)
XX XX
XX DE Murine BAD protein.
XX XX
XX KW BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
XX KW serine phosphorylation; post-translational modification; apoptosis;
XX KW signal transduction regulator; phosphoserine phosphatase; senescence;
XX KW immunodeficiency disease; neurodegenerative disease; infertility;
```

KW cancer, viral infection; lymphoproliferative condition; arthritis;
 KW inflammation; autoimmune diseases.
 XX Mus sp.
 OS WO9809643-A1.
 PN 12-MAR-1998.
 XX 09-SEP-1997; 97WO-US15871.
 XX 09-SEP-1996; 96US-0707868.
 XX (UNIW) UNIV WASHINGTON.
 PA Korschmeier SJ;
 PI WPI; 1998-207049/18.
 DR Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
 PT polypeptide - useful for modulation of apoptosis associated with,
 PT e.g. cancer and immunodeficiency diseases
 XX Claim 3; Fig 8; 61pp; English.
 PS This sequence represents a novel serine-phosphorylated protein, BAD
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
 CC phosphorylated in a post-translational modification and allows binding
 CC to the 14-3-3 protein which is a signal transduction regulator.
 CC Modulators of phosphorylated BAD, which act through inhibition/activation
 CC of a phosphoserine phosphatase, are useful for preventing/treating
 CC increased/decreased apoptosis in a cell. The increased apoptosis may
 CC result from immunodeficiency diseases, senescence, neurodegenerative
 CC disease, ischaemic cell death, reperfusion cell death, infertility and
 CC wound-healing. Decreased apoptosis may result from cancer, viral
 CC infection, lymphoproliferative conditions, arthritis, infertility,
 CC inflammation and autoimmune diseases. Measuring the amount of
 CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total
 CC BAD in a cell is useful for determining the apoptotic state of a cell.
 XX Sequence 204 AA;

Query Match 71.7%; Score 649; DB 19; Length 204;
 Best Local Similarity 75.6%; Pred. No. 9.1e-61;
 Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;
 QY 1 MFQIPFEPSEQEDSSAERGLGPGSPAGDGPSCGKHRRQAPGLLWDASHQQQPTSSSH 60
 DB 43 mtfqipefepseqedasatdrglpsitedqp---gpy--lapgllgslnhqggraatsnsh 97
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLMWAQRYGRELRRMSDE 120
 DB 98 hggagamestrsrhssypagteedegmeelsprgrsrsappnlwaqrygrellrmsde 157
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLRGSSAPSQ 168
 DB 158 fegsf-kglprpksgatqmrqsagwttriqswdwnrlngkggstpsq 204

RESULT 10
 AAB70369
 ID AAB70369 standard; protein; 204 AA.
 XX AAB70369;
 XX 02-MAY-2001 (first entry)
 XX Longer murine BAD mutant amino acid sequence SEQ ID NO:2.

Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX Mus musculus.
 OS Synthetic.
 XX WO200110888-A1.
 PN 15-FEB-2001.
 XX 30-MAY-2000; 2000WO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 PA Zhou X;
 PI WPI; 2001-138734/14.
 DR New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX Claim 4; Page 148; 157pp; English.
 PS The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC nootropic, antiischaemic, vulnerary, cytostatic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed longer murine BAD mutant amino acid sequence from the present
 CC invention.

Sequence 204 AA;
 Query Match 71.7%; Score 649; DB 22; Length 204;
 Best Local Similarity 75.6%; Pred. No. 9.1e-61;
 Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;
 QY 1 MFQIPFEPSEQEDSSAERGLGPGSPAGDGPSCGKHRRQAPGLLWDASHQQQPTSSSH 60
 DB 43 mtfqipefepseqedasatdrglpsitedqp---gpy--lapgllgslnhqggraatsnsh 97
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSPFRGRSRAPPNLMWAQRYGRELRRMSDE 120
 DB 98 hggagamestrsrhssypagteedegmeelsprgrsrsappnlwaqrygrellrmsde 157
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDNLRGSSAPSQ 168
 DB 158 fegsf-kglprpksgatqmrqsagwttriqswdwnrlngkggstpsq 204

RESULT 11
 AAW61317
 ID AAW61317 standard; Protein; 204 AA.
 XX

AAW61317;
07-OCT-1998 (first entry)
Mutant BCL-XL/BCL-2 associated cell death regulator #2.
Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
serine substituted mutant; apoptosis; cancer; viral infection.
Mus sp.
Synthetic.
W09817682-A1.
30-APR-1998.
17-OCT-1997; 97WO-US19175.
18-OCT-1996; 96US-0733505.
(UNIW) UNIV WASHINGTON.
Korsmeyer SJ;
WPI; 1998-261422/23.
N-PSDB; AAV27835.
New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection
Claim 7; Page 60; 95pp; English.
The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
death regulator) proteins, having an amino acid other than Ser at
position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
present sequence represents a mutant BAD protein. Also described are: (1)
fragments of mutant BAD protein able to decrease cell viability; (2)
fusion proteins of mutant BAD with a heterologous polypeptide that
increases intracellular delivery. Mutant BAD proteins are used to treat
or prevent diseases associated with reduced apoptosis, e.g. cancer,
viral infection, lymphoproliferation, arthritis, infertility,
inflammation and autoimmune disease. Polynucleotide sequences encoding
mutant BAD proteins can be used similarly by gene therapy or to produce
transgenic animals for use as disease models or in drug screening. BAD
proteins phosphorylated at specified Ser are used to screen for enhancers
and inhibitors of serine-phosphatase. Inhibitors are potentially useful
in treatment of excessive apoptosis such as AIDS, neurodegeneration,
aging or ischaemic cell death. The apoptotic status of cells is
determined by measuring relative amounts of phosphorylated and non-
phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
greater death-promoting activity than wild-type BAD which can become
phosphorylated on the specified Ser, forming a product that does not
heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
proteins in the cytosol, thus promoting cell survival. The mutants with
Ser substituted cannot bind 14-3-3.
Sequence 204 AA;
Query Match 71.4%; Score 646; DB 19; Length 204;
Best Local Similarity 75.0%; Pred. No. 1.9e-60;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQEQPTSSSH 60
DB 43 mtfqipefseqedasatdrglgsitedqp---gpy--lapglglnlhqggraatnsh 97
QY 61 HGGAGAVETRSHSSYPAGTDEGMEEPSPFRGSRSPAPNLWAAQRYGRELRRMSDE 120
DB 98 hggagavetrshssypagtedegmeelspfrgsraapnlwaaqrygrelrrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

Db 158 fegsf-kglprpksgagtatmrqsagwtlrlqsgwwdrnlkgsgstpsq 204
RESULT 12
AAW61316
ID AAW61316 standard; Protein; 204 AA.
XX
AC AAW61316;
XX
DT 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #1.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
PN W09817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1998-261422/23.
DR N-PSDB; AAV27834.
XX
PT New mutant BAD polypeptide with phosphorylatable serine replaced -
useful for, e.g. treating reduced apoptosis such as in cancer or
viral infection
XX
PS Claim 7; Page 59; 95pp; English.
XX
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
death regulator) proteins, having an amino acid other than Ser at
position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
present sequence represents a mutant BAD protein. Also described are: (1)
fragments of mutant BAD protein able to decrease cell viability; (2)
fusion proteins of mutant BAD with a heterologous polypeptide that
increases intracellular delivery. Mutant BAD proteins are used to treat
or prevent diseases associated with reduced apoptosis, e.g. cancer,
viral infection, lymphoproliferation, arthritis, infertility,
inflammation and autoimmune disease. Polynucleotide sequences encoding
mutant BAD proteins can be used similarly by gene therapy or to produce
transgenic animals for use as disease models or in drug screening. BAD
proteins phosphorylated at specified Ser are used to screen for enhancers
and inhibitors of serine-phosphatase. Inhibitors are potentially useful
in treatment of excessive apoptosis such as AIDS, neurodegeneration,
aging or ischaemic cell death. The apoptotic status of cells is
determined by measuring relative amounts of phosphorylated and non-
phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
greater death-promoting activity than wild-type BAD which can become
phosphorylated on the specified Ser, forming a product that does not
heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
proteins in the cytosol, thus promoting cell survival. The mutants with
Ser substituted cannot bind 14-3-3.
XX
SQ Sequence 204 AA;
Query Match 71.0%; Score 643; DB 19; Length 204;
Best Local Similarity 74.4%; Pred. No. 3.9e-60;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;
QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQEQPTSSSH 60

Db 43 mfgipefepesqedasatdrglpsitedqp---gpy--lapgllgnsihqggraatsnsh 97
QY 61 HGAGAVEIRSRSSYPAGTEDEGMEEPSPPFRGRSRAPPNLMWAAQRYGRELRRMSDE 120
Db 98 hggagametrsrhsaypagteedegmeelspfrgrsraappulwaagyrygrelrrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWDNRNLGRGSSAPSQ 168
Db 158 fegsf-kglprksagatqmrqsagwttriigswdwnlrgkggstpsq 204

RESULT 13
AAW61318
ID AAW61318 standard; Protein; 204 AA.
XX AAW61318;
XX
DT 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
XX Synthetic.
XX
PN WO9817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1998-361422/23.
DR N-PSDB; AAV27836.
XX
PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
PS Claim 7; Page 60-61; 95pp; English.
XX
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.

SQ Sequence 204 AA;
Query Match 71.0%; Score 643; DB 19; Length 204;
Best Local Similarity 74.4%; Pred. No. 3.9e-60;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDQPSGSGKHHRQAPGLLWDASHQQEQPTSSSH 60
Db 43 mfgipefepesqedasatdrglpsitedqp---gpy--lapgllgnsihqggraatsnsh 97
QY 61 HGAGAVEIRSRSSYPAGTEDEGMEEPSPPFRGRSRAPPNLMWAAQRYGRELRRMSDE 120
Db 98 hggagametrsrhsaypagteedegmeelspfrgrsraappulwaagyrygrelrrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATOMROSSWTRVFQSWDNRNLGRGSSAPSQ 168
Db 158 fegsf-kglprksagatqmrqsagwttriigswdwnlrgkggstpsq 204

RESULT 14
AAW61319
ID AAW61319 standard; Protein; 59 AA.
XX AAW61319;
XX
DT 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #4.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
XX Synthetic.
XX
PN WO9817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1998-361422/23.
DR N-PSDB; AAV27837.
XX
PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
PS Claim 8; Page 73; 95pp; English.
XX
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

XX
SQ Sequence 59 AA;

Query Match 34.7%; Score 314; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSDEF 121
DB 1 gagaveirsrhssypagteddegmgpepsppfrgrsrappnlwaaqrygrelrmsdef 59

RESULT 15
AAW61320
ID AAW61320 standard; Protein; 59 AA.
XX
AC AAW61320;
XX
DT 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #5.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX
PN W09817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1998-261422/23.
DR N-PSDB; AAV27838.
XX
PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
PS Claim 8; Page 73; 95pp; English.
XX
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have greater death-promoting activity than wild-type BAD which can become phosphorylated on the specified Ser, forming a product that does not heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with Ser substituted cannot bind 14-3-3.

XX
SQ Sequence 59 AA;

Query Match 34.7%; Score 314; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPSPPFRGRSRAPPNLWAAQRYGRELRMSDEF 121
DB 1 gagaveirsrhssypagteddegmgpepsppfrgrsrappnlwaaqrygrelrmsdef 59

Search completed: October 9, 2001, 15:53:27
Job time: 203 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:59:30 ; Search time 239.36 Seconds
(without alignments)
155.708 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIPEFPESEQEDSSAER.....RVFSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	905	100.0	168	1	PCT-US00-11864-1
2	905	100.0	168	17	US-09-375-257-2
3	905	100.0	168	17	US-09-376-154-2
4	905	100.0	168	18	US-09-410-372-1
5	905	100.0	168	18	US-09-456-357-32
6	905	100.0	168	19	US-09-580-523-1
7	905	100.0	168	19	US-09-587-473-21
8	744	82.2	168	12	US-08-883-731-2
9	744	82.2	168	18	US-09-410-372-7
10	673	74.4	125	23	US-60-197-873-16338

11	649	71.7	162	1	PCT-US00-11864-3	Sequence 3, Appli
12	649	71.7	162	19	US-09-580-523-3	Sequence 3, Appli
13	649	71.7	204	1	PCT-US00-11864-2	Sequence 2, Appli
14	649	71.7	204	1	PCT-US97-15871-1	Sequence 1, Appli
15	649	71.7	204	1	PCT-US97-15871A-1	Sequence 1, Appli
16	649	71.7	204	1	PCT-US98-19765-41	Sequence 41, Appli
17	649	71.7	204	11	US-08-707-868-1	Sequence 1, Appli
18	649	71.7	204	11	US-08-733-505-1	Sequence 1, Appli
19	649	71.7	204	13	US-08-946-039-41	Sequence 41, Appli
20	649	71.7	204	19	US-09-580-523-2	Sequence 2, Appli
21	646	71.4	204	11	US-08-733-505-12	Sequence 12, Appli
22	646	71.4	204	11	US-08-733-505-13	Sequence 13, Appli
23	646	71.4	204	17	US-09-375-257-3	Sequence 3, Appli
24	646	71.4	204	17	US-09-376-154-3	Sequence 3, Appli
25	643	71.0	204	11	US-08-733-505-14	Sequence 14, Appli
26	643	71.0	567	20	US-09-639-245-4	Sequence 4, Appli
27	334	36.9	63	1	PCT-US97-15871A-12	Sequence 12, Appli
28	334	36.9	63	1	PCT-US98-19765-42	Sequence 42, Appli
29	334	36.9	63	13	US-08-946-039-42	Sequence 42, Appli
30	314	34.7	59	11	US-08-733-505-5	Sequence 5, Appli
31	311	34.4	59	11	US-08-733-505-56	Sequence 56, Appli
32	311	34.4	59	11	US-08-733-505-57	Sequence 57, Appli
33	308	34.0	59	11	US-08-733-505-58	Sequence 58, Appli
34	133	14.7	26	1	PCT-US00-11864-4	Sequence 4, Appli
35	133	14.7	26	1	PCT-US99-25285-5	Sequence 5, Appli
36	133	14.7	26	15	US-09-184-168A-5	Sequence 4, Appli
37	133	14.7	26	19	US-09-580-523-4	Sequence 4, Appli
38	132	14.6	25	20	US-09-656-399-10	Sequence 10, Appli
39	132	14.6	25	20	US-09-656-399A-10	Sequence 10, Appli
40	132	14.6	25	21	US-09-716-395-20	Sequence 20, Appli
41	129	14.3	25	20	US-09-656-399-17	Sequence 17, Appli
42	129	14.3	25	20	US-09-656-399A-17	Sequence 17, Appli
43	129	14.3	25	21	US-09-716-395-26	Sequence 26, Appli
44	128	14.1	25	20	US-09-656-399-15	Sequence 15, Appli
45	128	14.1	25	20	US-09-656-399-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1

PCT-US00-11864-1

; Sequence 1, Application PC/TUS0011864

; GENERAL INFORMATION:

; APPLICANT: APOPTOSIS TECHNOLOGY, INC.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,

; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS

; TITLE OF INVENTION: THAT REGULATE APOPTOSIS

; FILE REFERENCE: F137122

; CURRENT APPLICATION NUMBER: PCT/US00/11864

; CURRENT FILING DATE: 2000-05-30

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 1

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-11864-1

Query Match	100.0%;	Score 905;	DB 1;	Length 168;
Best Local Similarity	100.0%;	Pred. No. 5.3e-71;		
Matches 168;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFQIPEFPESEQEDSSAERGLGPSAGDGGSGSKHHRQAPGLLWDASHQOQPTSSSH	60	
Db	1	MFQIPEFPESEQEDSSAERGLGPSAGDGGSGSKHHRQAPGLLWDASHQOQPTSSSH	60	
Qy	61	HGGAGAVEIRSHSSYPAGTDEGCGEPPFGRGRSAPPNLWAAORYGRELARMDSDE	120	
Db	61	HGGAGAVEIRSHSSYPAGTDEGCGEPPFGRGRSAPPNLWAAORYGRELARMDSDE	120	
Qy	121	FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ	168	

Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
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RESULT 2

US-09-375-257-2
; Sequence 2, Application US/09375257
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D1
; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-257-2

Query Match 100.0%; Score 905; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.3e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHKRAQGLLWDASHQEQPTSSSH 60
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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHKRAQGLLWDASHQEQPTSSSH 60
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QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120
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Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
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RESULT 3

US-09-376-154-2
; Sequence 2, Application US/09376154
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D2
; CURRENT APPLICATION NUMBER: US/09/376,154
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-376-154-2

Query Match 100.0%; Score 905; DB 17; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.3e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHKRAQGLLWDASHQEQPTSSSH 60
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QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120
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Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120
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QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||

RESULT 4

US-09-410-372-1
; Sequence 1, Application US/09410372
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-09-410-372-1

Query Match 100.0%; Score 905; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.3e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHKRAQGLLWDASHQEQPTSSSH 60
|||||
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120
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Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRRMSDE 120
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QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
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Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||

RESULT 5

US-09-456-357-32

; Sequence 32, Application US/09456357
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/09/456,357
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: 60/134,416
; EARLIER FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: 09/087,195
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/378,507
; EARLIER FILING DATE: 1995-01-26
; EARLIER APPLICATION NUMBER: 08/250,478
; EARLIER FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-357-32

Query Match 100.0%; Score 905; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.3e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHOQEQPTSSSH 60
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Db 61 HGGAGAVEIRSRHSYPAGTDEDCMGEEPPFRGRSRSPAPNLWAAQRYGRELRMSDE 120
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Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 6
US-09-580-523-1
; Sequence 1, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-523-1

Query Match 100.0%; Score 905; DB 19; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.3e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHOQEQPTSSSH 60
Qy 61 HGGAGAVEIRSRHSYPAGTDEDCMGEEPPFRGRSRSPAPNLWAAQRYGRELRMSDE 120
Db 61 HGGAGAVEIRSRHSYPAGTDEDCMGEEPPFRGRSRSPAPNLWAAQRYGRELRMSDE 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
RESULT 7
US-09-587-473-21
; Sequence 21, Application US/09587473
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Tsvetkov, Lyuben
; TITLE OF INVENTION: Protein Knockout Technology
; FILE REFERENCE: 44574-5047-WO
; CURRENT APPLICATION NUMBER: US/09/587,473
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/137,494
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-587-473-21

Query Match 100.0%; Score 905; DB 19; Length 168;
Best Local Similarity 100.0%; Pred. No. 5.3e-71;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHOQEQPTSSSH 60
Db 1 MFQIPEFPSEQDSSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHOQEQPTSSSH 60
Qy 61 HGGAGAVEIRSRHSYPAGTDEDCMGEEPPFRGRSRSPAPNLWAAQRYGRELRMSDE 120
Db 61 HGGAGAVEIRSRHSYPAGTDEDCMGEEPPFRGRSRSPAPNLWAAQRYGRELRMSDE 120
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 8
US-08-883-731-2
; Sequence 2, Application US/08883731
; GENERAL INFORMATION:
; APPLICANT: Zhu, Li
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation Cell Death
; FILE REFERENCE: D6120
; CURRENT APPLICATION NUMBER: US/08/883,731
; CURRENT FILING DATE: 1997-06-27
; EARLIER APPLICATION NUMBER: US 08/665,617
; EARLIER FILING DATE: 1996-06-18
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; LOCATION:
; OTHER INFORMATION: Protein encoded by the BBC6 gene.
US-08-883-731-2

Query Match 82.2%; Score 744; DB 12; Length 168;
Best Local Similarity 85.1%; Pred. No. 6.4e-57;
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMSDE 120
Db 61 HGGWCGDPESQPLLPRGDGRRDRGGGAQPFGRSRSPAPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRKPSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRKPSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 9
US-09-410-372-7
; Sequence 7, Application US/09410372
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-09-410-372-7

Query Match 82.2%; Score 744; DB 18; Length 168;
Best Local Similarity 85.1%; Pred. No. 6.4e-57;
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 60
Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMSDE 120
Db 61 HGGWCGDPESQPLLPRGDGRRDRGGGAQPFGRSRSPAPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRKPSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

Db 121 FVDSFKKGLPRKPSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 10
US-60-197-873-16338
; Sequence 16338, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Seyerin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81 US1 PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 16338
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-197-873-16338

Query Match 74.4%; Score 673; DB 23; Length 125;
Best Local Similarity 100.0%; Pred. No. 7.2e-51;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 60
Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMSDE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSF 125
Db 121 FVDSF 125

RESULT 11
PCT-US00-11864-3
; Sequence 3, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137/122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-3

Query Match 71.7%; Score 649; DB 1; Length 162;
Best Local Similarity 75.6%; Pred. No. 1.2e-48;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 60
Db 1 MFOIPEFPESEQEDSSAERGLGSPAGDGPSCGSKHHRQAPGLLWDASHQQEQPTSSSH 55
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPFRGRSRSPAPNLWAAQRYGRELRRMSDE 120

Db 56 HGGAGAMETRRSHSSYPAGTEDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 115
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 116 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGSTPSQ 162

RESULT 12
US-09-580-523-3
; Sequence 3, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-580-523-3

Query Match 71.7%; Score 649; DB 19; Length 162;
Best Local Similarity 75.6%; Pred. No. 1.2e-48;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLDASHOQEQPTSSSH 60
Db 1 MFQIPEFPSEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 55

QY 61 HGGAGAVEIRSHSSYPAGTDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120
Db 56 HGGAGAMETRRSHSSYPAGTEDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 115

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 116 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGSTPSQ 162

RESULT 13
PCT-US00-11864-2
; Sequence 2, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-2

Query Match 71.7%; Score 649; DB 1; Length 204;
Best Local Similarity 75.6%; Pred. No. 1.6e-48;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLDASHOQEQPTSSSH 60
Db 43 MFQIPEFPSEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97

QY 61 HGGAGAVEIRSHSSYPAGTDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120

Db 98 HGGAGAMETRRSHSSYPAGTEDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 158 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGSTPSQ 204

RESULT 14
PCT-US97-15871-1
; Sequence 1, Application PC/TUS9715871
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/15871
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-15871-1

Query Match 71.7%; Score 649; DB 1; Length 204;
Best Local Similarity 75.6%; Pred. No. 1.6e-48;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLDASHOQEQPTSSSH 60
Db 43 MFQIPEFPSEQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97

QY 61 HGGAGAVEIRSHSSYPAGTDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120
Db 98 HGGAGAMETRRSHSSYPAGTEDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 157

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 158 FEGSF-KGLPRPKSAGTATQMRQSSAGWTRIIQSWWDRNLGKGSTPSQ 204

RESULT 15
PCT-US97-15871A-1
; Sequence 1, Application PC/TUS9715871A
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE

Search completed: October 9, 2001, 16:07:48
Job time: 498 sec


```
; SEQ ID NO 2762
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (146)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (169)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-2762
```

```
Query Match 95.5%; Score 864; DB 1; Length 201;
Best Local Similarity 98.2%; Pred. No. 5.2e-54;
Matches 160; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
Db 9 MFQIPFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 68
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRAPPNLAQAQRYGRELRRMSDE 120
Db 69 HGCAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRAPPNLAQAQRYGRELRRMSDE 128
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGS 163
Db 129 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGS 171
```

```
RESULT 3
US-09-834-366-16338
; Sequence 16338, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81.052.REG
; CURRENT APPLICATION NUMBER: US/09/834,366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 16338
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-366-16338
```

```
Query Match 74.4%; Score 673; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 8.5e-41;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
Db 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRAPPNLAQAQRYGRELRRMSDE 120
Db 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRAPPNLAQAQRYGRELRRMSDE 120
```

```
QY 121 FVDSF 125
Db 121 FVDSF 125
```

RESULT 4

```
US-09-922-378-3
; Sequence 3, Application US/09922378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-922-378-3
```

```
Query Match 71.4%; Score 646; DB 5; Length 204;
```

```
Best Local Similarity 75.0%; Pred. No. 1.1e-38;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
```

```
QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLWDASHQEQPTSSSH 60
Db 43 MFQIPFEPSEQEDASATDRGLGSLTQDQ---GPY--LAPGLLGSNIHQQGRAATNSH 97
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRAPPNLAQAQRYGRELRRMSDE 120
Db 98 HGCAGAVEIRSRHSSYPAGTDEDEGMEEPSPPRGRSRAPPNLAQAQRYGRELRRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGSAPSQ 168
Db 158 FEGSF-KGLPRPKSAGTATQMRQSSSWTRVFQSWDNLGRGSAPSQ 204
```

RESULT 5

```
US-09-758-466-434
; Sequence 434, Application US/09758466
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM036
; CURRENT APPLICATION NUMBER: US/09/758,466
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 434
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (120)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (129)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (136)
```

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-466-434

Query Match 24.6%; Score 223; DB 5; Length 142;
Best Local Similarity 45.1%; Pred. No. 4.3e-09;
Matches 60; Conservative 8; Mismatches 37; Indels 28; Gaps 7;
Qy 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLW-----DA 48
Db 26 MFQIPFEPSEQEDSSAERGLGSPAGRGP-----QAPASIIARQASCGTPSPAG 77
Qy 49 SHQOQPTSSHHGAGAVEIRSRSSYPAGTEDDEGMGEPPSPFRGRSRAPPNLWAAQ 108
Db 78 AANQOOP--SWRRWCGDPE---SXQFYFAGTEDDEGNGRSPA-LLGPXGFGPPT-FCXT 130
Qy 109 RYGRRLRMSDEF 121
Db 131 GYGRN-XELNDDF 142

RESULT 6
US-09-758-466-716
; Sequence 716, Application US/09758466
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM036
; CURRENT APPLICATION NUMBER: US/09/758,466
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 716
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (72)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (125)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (153)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (166)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (170)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (178)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (199)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (202)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (206)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-466-716

Query Match 13.5%; Score 122.5; DB 5; Length 211;
Best Local Similarity 27.3%; Pred. No. 0.078;
Matches 44; Conservative 15; Mismatches 75; Indels 27; Gaps 5;
Qy 19 ERGLSPAGDPSGSGKHHRQAPGLL-WDASHQDEQPTSSS-----HHGAGAVEIR 70
Db 65 ORGAWAQPQTGPGSGKHHRQAPGCGTPVTSRSQPAAAIMEALGLWRSGVATAPTR 124
Qy 71 SRHSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEFV-----DSEK 126
Db 125 XRRTT-----KMGGRSPAPFGAVRAXAPQLGSLXALWRAPEMSDDXWILXRRDFFA 176
Qy 127 KGLPRPKSAGTATMRQSSSWTRVFQSWMDRLNLGRSSAPS 167
Db 177 RXARAHNQC-----KFHWKHFSLVGYXRNXXGQGFAPS 210

RESULT 7
US-09-760-476-1456
; Sequence 1456, Application US/09760476
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC015
; CURRENT APPLICATION NUMBER: US/09/760,476
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2602
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1456
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-476-1456

Query Match 11.3%; Score 102.5; DB 5; Length 123;
Best Local Similarity 62.9%; Pred. No. 1.1;
Matches 22; Conservative 2; Mismatches 4; Indels 7; Gaps 2;
Qy 77 PAGTEDDEGMGEPPSPFRGRSRAPPN-----LW 105
Db 83 PRGTEDDEGMGEPPSPFR-RARARRPQIGSTALW 116

RESULT 8
PCT-US01-08631-54396
; Sequence 54396, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54396
; LENGTH: 1401
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (199)...(248)
; OTHER INFORMATION: Eukaryotic RNA polymerase II heptapeptide repeat proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL001152, p-val
; OTHER INFORMATION: 7.221e-09, raw score of 3.12
PCT-US01-08631-54396

```
Query Match      11.1%; Score 100.5; DB 1; Length 1401;
Best Local Similarity 26.0%; Pred. No. 21;
Matches 34; Conservative 8; Mismatches 62; Indels 27; Gaps 3;

QY 15 SSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHHQEQPTSSHHGGAGAVEIRSRHS 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 599 TSAHHHGSAPPT-----SAHHGSAP-----PPTSAHHHGSAPPTSAHHHG 641
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 75 SYPAGTEDDEGMEEPSFPRGRSRAPPNLLAAQRYGRELRRMSDEVD----- 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 642 SAPPTSAHQYHGSAPPTSAHHHDSAPPTSAHHHGSAPRPTSAHHHGSAPPLTSAYQ 701
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 125 FKKGLPRPKSA 135
   : : : : :
Db 702 YHDSAPRPTSA 712

RESULT 9
US-09-902-540-10164
; Sequence 10164, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10164
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10164

Query Match      10.6%; Score 95.5; DB 5; Length 743;
Best Local Similarity 27.5%; Pred. No. 24;
Matches 44; Conservative 17; Mismatches 58; Indels 41; Gaps 8;

QY 2 FQIPEFSPQEDSSAERGLGPS-----PAGDPSGSGKHHRQAPGLLWDA-SHQEQ 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 WEAPPGEAASVRQSSRTSMGPRRTSAAPVAVE-PDEQGE-----WDAPSGIEEA 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 55 PTSSSHHGGAGAVEIRSRHSYPAGTE-----DDEGMEEPSFPRGRSRSA----- 100
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 PPPRRRTSA-----ELRRPSNSTQIARTSSRSDLSRTGMGEPPTPPRRSATRAAQIVE 437
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 101 ----PNNLMAAQRYGREL-RMSDEFVDSFKGLPRPKSA 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 438 DPGPPFSRSRSMVAADVETRMEDDELDDERTMLPPEPA 477
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-760-461-53
; Sequence 53, Application US/09760461
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT244
; CURRENT APPLICATION NUMBER: US/09/760,461
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      10.3%; Score 93.5; DB 5; Length 535;
Best Local Similarity 25.0%; Pred. No. 23;
Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8;

QY 9 PSQEDSSSAERGLGSPAGDPSGSGKHHRQA-----PGLLDASHHQEQPTSSSH 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 PAKPEQGSSASR---PVPASRGKTKLCKGRQAPPGPPARFPRIWSASPPRAPSSTPC 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 HGGAGAVEIRSRHSYPAGTEDDEGMEEPSFPRGRSRAPPNLLAAQRYGRELRRMSDE 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 PGGA-----VREDTYPVGTQG-----VPSP--ALAQGGPQGSWRFLW----- 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVF---QSWMDRLNLR 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 -----NSMPR-----LPTDLDEGPMFRHYDFRQSCWRAISQ 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-760-485-758
; Sequence 758, Application US/09760485
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: FJ217
; CURRENT APPLICATION NUMBER: US/09/760,485
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 758
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (344)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (512)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-485-758

Query Match      10.3%; Score 93.5; DB 5; Length 535;
Best Local Similarity 25.0%; Pred. No. 23;
Matches 41; Conservative 17; Mismatches 57; Indels 49; Gaps 8;

QY 9 PSQEDSSSAERGLGSPAGDPSGSGKHHRQA-----PGLLDASHHQEQPTSSSH 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 PAKPEQGSSASR---PVPASRGKTKLCKGRQAPPGPPARFPRIWSASPPRAPSSTPC 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 HGGAGAVEIRSRHSYPAGTEDDEGMEEPSFPRGRSRAPPNLLAAQRYGRELRRMSDE 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 403 PGGA-----VREDTYPVGTQG-----VPSP--ALAQGGPQGSWRFLW----- 438
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVF---QSWMDRLNLR 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 -----NSMPR-----LPTDLDEGPMFRHYDFRQSCWRAISQ 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

FEATURE:
; NAME/KEY: SITE
; LOCATION: (236)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (344)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (512)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-461-53
```


RESULT 15

PCT-US01-08631-44993
; Sequence 44993, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44993
; LENGTH: 1475
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1475)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-44993

Query Match 10.1%; Score 91.5; DB 1; Length 1475;
Best Local Similarity 33.3%; Pred No. 93;
Matches 41; Conservative 8; Mismatches 49; Indels 25; Gaps 8;
QY 5 PEFEPSEQEDSSAERGLGSPAGDG-PSGS-GKHHRQAPGLIWDASHQOQPTSSSHHG 62
Db 757 PAAAPPSRE-GRSAERGWC-PAGPGAPRGXRGGRAGAP-----QHPPSRASQRG 805
QY 63 GAGAVEIRSRHS-----SYPAGTEDDEGMGEPEPFRGRSRKSPPNLWAAQRYGRELR 115
Db 806 AAGAAPXRAVHSRKLTFRARHLAAGLAGQPCRPDPVLLRG----APPPC-APARHGASAR 860
QY 116 RMS 118
Db 861 APS 863

Search completed: October 9, 2001, 16:08:31
Job time: 381 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:50:05 ; Search time 25.99 Seconds
(without alignments)
133.097 Million cell updates/sec

Title: US-09-580-523-1

Perfect score: 905

Sequence: 1 MFQIPEFSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/iaa/PCrUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	905	100.0	168	2	US-08-717-123-2
2	905	100.0	168	3	US-08-985-335-1
3	751	83.0	166	1	US-08-665-617-2
4	744	82.2	168	3	US-08-985-335-7
5	649	71.7	204	1	US-08-333-565-2
6	649	71.7	204	2	US-08-661-479-2
7	649	71.7	204	2	US-08-733-505A-1
8	646	71.4	204	2	US-08-733-505A-12
9	646	71.4	204	2	US-08-733-505A-13
10	646	71.4	204	2	US-08-717-123-3
11	643	71.0	204	2	US-08-733-505A-14
12	314	34.7	59	2	US-08-733-505A-55
13	311	34.4	59	2	US-08-733-505A-56
14	311	34.4	59	2	US-08-733-505A-57
15	308	34.0	59	2	US-08-733-505A-58
16	116	12.8	23	1	US-08-333-565-10
17	116	12.8	23	2	US-08-661-479-10
18	97	10.7	2509	2	US-08-149-097D-35
19	96.5	10.7	1182	4	US-09-041-886-21
20	90	9.9	434	1	US-08-337-602-3
21	90	9.9	434	3	US-08-558-135-3
22	90	9.9	2237	1	US-08-455-543A-48
23	90	9.9	2237	2	US-08-223-305C-48
24	90	9.9	2337	3	US-08-713-118-2
25	90	9.9	2337	4	US-09-452-007-2
26	90	9.9	2339	1	US-08-455-543A-47
27	90	9.9	2339	2	US-08-223-305C-47

28	88.5	9.8	393	2	US-09-026-587-3	Sequence 3, Appli
29	88.5	9.8	393	2	US-09-227-420-3	Sequence 3, Appli
30	87	9.6	418	2	US-09-026-587-1	Sequence 1, Appli
31	87	9.6	418	2	US-09-227-420-1	Sequence 1, Appli
32	86.5	9.6	378	2	US-08-986-217-6	Sequence 6, Appli
33	86	9.5	16	1	US-08-333-565-26	Sequence 26, Appli
34	86	9.5	16	2	US-08-661-479-26	Sequence 2, Appli
35	86	9.5	591	3	US-09-082-737-2	Sequence 2, Appli
36	85	9.4	380	2	US-09-026-587-4	Sequence 4, Appli
37	85	9.4	380	2	US-09-227-420-4	Sequence 4, Appli
38	84.5	9.3	1159	2	US-08-956-242-13	Sequence 13, Appli
39	84.5	9.3	1159	3	US-09-351-215-13	Sequence 13, Appli
40	84.5	9.3	1159	4	US-09-226-012-2	Sequence 2, Appli
41	84.5	9.3	1159	4	US-09-226-012-4	Sequence 4, Appli
42	84	9.3	16	1	US-08-333-565-17	Sequence 17, Appli
43	84	9.3	16	2	US-08-661-479-17	Sequence 17, Appli
44	84	9.3	575	3	US-08-922-865-2	Sequence 2, Appli
45	82	9.1	424	2	US-08-592-214A-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match 100.0%; Score 905; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 4.4e-86;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHHRRQAPGLLDWASHQEQPTSSSH 60
DB 1 MFQIPEFSEQEDSSAERGLGSPAGDPSGSGKHHRRQAPGLLDWASHQEQPTSSSH 60

Qy	61	HGCAGAVETIRSRHSSYPAGTETDEGNGEEPSFGRGRSAPPNLWAAQRYGRELRMSDE	120
Db	61	HGCAGAVETIRSRHSSYPAGTETDEGNGEEPSFGRGRSAPPNLWAAQRYGRELRMSDE	120

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
 |||||
 Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

```

RESULT      2
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

```

Query Match	100.0%	Score 905;	DB 3;	Length 168;
Best Local Similarity	100.0%	Pred. No. 4.4e-86;		
Matches 168;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY	1	MFQIPEPPESEQEDSSAERGLGPGSPAGDGPSSGSKHHKRAQPCLLWDASHQEQEPSSSH	60
Db	1	MFQIPEPPESEQEDSSAERGLGPGSPAGDGPSSGSKHHKRAQPCLLWDASHQEQEPSSSH	60
QY	61	HGAGAVEISRHSSTYPAGTDEDEGMEEPSPPRGSRSPAPNLAQAQRYGRELRRMSDE	120
Db	61	HGAGAVEISRHSSTYPAGTDEDEGMEEPSPPRGSRSPAPNLAQAQRYGRELRRMSDE	120
QY	121	FVDSFKKGLPRPKSAGTATQMRSSSWTRVFQSWDNRNLGRGSSAPSQ	168

db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168

RESULT 3
 US-08-665-617-2
 ; Sequence 2, Application US/08665617
 ; Patent No. 5663316
 ; GENERAL INFORMATION:
 ; APPLICANT: Xudong, Yin
 ; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/665,617
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saliwanchik, David R.
 ; REGISTRATION NUMBER: 31,794
 ; REFERENCE/DOCKET NUMBER: CL-8
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (352) 375-8100
 ; TELEFAX: (352) 372-5800
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 166 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-665-617-2

Query Match	83.0%	Score 751;	DB 1;	Length 166;
Best Local Similarity	84.0%	Pred. NO. 3.3e-70;		
Matches 147;	Conservative	3;	Mismatches 9;	Indels 16;
				Gaps 3;

Qy	1	MFQIPEEPSEQEDSSAERGLGPGSDGPGSGKHHRQAPG-----LWMDASHQOE	53
Db	1	MFQIPEEPSEQEDSSAERG-WRSPAGTGP-----QAPASIIARQVWLWDASHQOE	51
Qy	54	QPTSSSHHGAGAGAVEIRSRHSSYPAGTDEDEGGEPSPPFRGSRSAPNLWAAQRYGRE	113
Db	52	QPTSSSHHGAGAGAVEIRSRHSSYPAGTDEDEGGEPSPPFRGARARPPNLWAAQRYGRE	111
Qy	114	LRRMSDEFVSFKKGLPRPKSAGTATQMROSSWTRVFOSWMDRNLGRSSAPSQ	168
Db	112	LRRMSDEFVSFKKGLPRPKSAGTATQMROSSWTRVFOSWMDRNLGRGTAAPSQ	166

```

RESULT          4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION

```

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSPSQ 168

APPLICANT: COLLEY, WILL C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION

* NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7

Query Match 82.2%; Score 744; DB 3; Length 168;
Best Local Similarity 85.18; Pred. No. 1.8e-69;
Matches 143; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60
|||||
Db 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60
Qy 61 HGGAGAVIRSHSYSPAGTDEGCMGEEPPFRGSRSPAPNLWAAQRYGRELRRMSDE 120
|||
Db 61 HGGRWCGDPEPQQLPRGDDGRRDGGQAQPFGRGSRSPAPNLWAAQRYGRELRRMSDE 120
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRNLGRGSSAPSQ 168

RESULT 5
US-08-333-565-2
Sequence 2, Application US/083333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."
US-08-333-565-2

Query Match 71.7%; Score 649; DB 1; Length 204;
Best Local Similarity 75.6%; Pred. No. 1.4e-59;
Matches 127; Conservative 12; Mismatches 23; Indels 6; Gaps 3;
Qy 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQEQPTSSSH 60
|||||
Db 43 MFQIPEFPEPSEQEDASATDRGLGSLTDEQP---GPY--LAPGLLGSNIHQGRAATNSH 97
Qy 61 HGGAGAVIRSHSYSPAGTDEGCMGEEPPFRGSRSPAPNLWAAQRYGRELRRMSDE 120
|||||
Db 98 HGGAGAMETRSHSYSPAGTDEGMEELSPFRGSRSPAPNLWAAQRYGRELRRMSDE 157
Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRNLGRGSSAPSQ 168
|||
Db 158 FEGSPF-KGLPRPKSAGTATQMRQSGAGWTRIQSWMDRNLGKGSTPSQ 204

RESULT 6
US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565

Db 43 MFQIPEPESQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97
QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMEEPSPFGRSRSPAPNLAQRYGRELRRMSDE 120
Db 98 HGGAGAMETRSRHSYPAGTDEGMEELSPFGRSRSPAPNLAQRYGRELRRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 158 FEGSF-KGLPRKSAGTATQMRQSGWTRIIQSWWDRNLGRKGSTPSQ 204

RESULT 9

US-08-733-505A-13
; Sequence 13, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 2.9e-59;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESQEDSSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
Db 43 MFQIPEPESQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97
QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMEEPSPFGRSRSPAPNLAQRYGRELRRMSDE 120
Db 98 HGGAGAMETRSRHSYPAGTDEGMEELSPFGRSRSPAPNLAQRYGRELRRMSDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 158 FEGSF-KGLPRKSAGTATQMRQSGWTRIIQSWWDRNLGRKGSTPSQ 204

RESULT 10

US-08-717-123-3

; Sequence 3, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-717-123-3

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 2.9e-59;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESQEDSSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
Db 43 MFQIPEPESQEDASATDRGLGSLTEDQP---GPY--LAPGLLGSNIHQGRAATNSH 97
QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMEEPSPFGRSRSPAPNLAQRYGRELRRMSDE 120
Db 98 HGGAGAMETRSRHSYPAGTDEGMEELSPFGRSRSPAPNLAQRYGRELRRMTDE 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 158 FEGSF-KGLPRKSAGTATQMRQSGWTRIIQSWWDRNLGRKGSTPSQ 204

RESULT 11

US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-14

Query Match 71.0%; Score 643; DB 2; Length 204;
Best Local Similarity 74.4%; Pred. No. 5.9e-59;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;

QY 1 MQQIFEFSEQDSSAERGLGPGSPAGDGPSSGKHHRQAPGLLWDASHQEQPTSSSH 60
DB 43 MQQIFEFSEQDASATDGLGPSITDQP--GPG--LAPGLLGSNIHQGGRATNSH 97
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120
DB 98 HGGAGAMETRSRHSAYPAGTEDEGMGEELSPPFRGRSRAPPNLWAAQRYGRELRRMSDE 157
QY 121 FVDSFKGLPRKPSAGTATQMSQSWTRVFSQWMDRNLGRSSAPFSQ 168
DB 158 FEGSF-KGLPRKPSAGTATQMSQAGWTRIQSWMDRNLKGGSTPSQ 204

RESULT 12
US-08-733-505A-55
; Sequence 55, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-56

Query Match 34.4%; Score 311; DB 2; Length 59;
Best Local Similarity 98.3%; Pred. No. 2e-25;
Matches 58; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 121
DB 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

RESULT 13
US-08-733-505A-56
; Sequence 56, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-55

Query Match 34.7%; Score 314; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 9.8e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 121
DB 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

RESULT 14
US-08-733-505A-57
; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
```

; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-57

Query Match 34.4%; Score 311; DB 2; Length 59;
Best Local Similarity 98.3%; Pred. No. 2e-25;
Matches 58; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 121
|||||
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 59

RESULT 15
US-08-733-505A-58
; Sequence 58, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:

; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-58

Query Match 34.0%; Score 308; DB 2; Length 59;
Best Local Similarity 96.6%; Pred. No. 4.1e-25;
Matches 57; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 121
|||||
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPRGRSRAPPNLWAAQRYGRELRMSDEF 59

Search completed: October 9, 2001, 15:52:36
Job time: 151 sec

Qy 1 QSSWTRVFQSWDRNLGRSSAPSQ 26
 |||
 db 143 OSSWTRVFQSWDRNLGRSSAPSQ 168


```

RESULT      9
ID          074309
ID          074309      PRELIMINARY;      PRT;      807 AA.
AC          074309;
DT          01-NOV-1998      (TEMBLrel. 08, Created)
DT          01-NOV-1998      (TEMBLrel. 08, Last sequence update)
DT          01-MAR-2001      (TEMBLrel. 16, Last annotation update)
DE          H1STONE TRANSCRIPTIONAL REGULATOR HOMOLOG..
GN          SPBC15D4.03..
OS          Schizosaccharomyces pombe (Fission yeast).
OC          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC          Schizosaccharomycetales; Schizosaccharomycetaceae;
OC          Schizosaccharomycetes.
OX          NCBI_TaxID=4896;
RN          [1]
RP          SEQUENCE FROM N.A.
RC          STRAIN=972H-;
RA          Lyne M., Rajadream M.A., Barrell B.G., Lucas M., Gaillardin C.A.
RL          Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR          EMBL; AL031349; CAA20478.1; -.
DR          InterPro; IPR001680; -.
DR          Pfam; PF00400; WD40; 5.
DR          PROSITE; PS00678; WD REPEATS; UNKNOWN 1.

```

DR SMART; SM00320; WD40; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 807 AA; 90432 MW; B8BFB73852EB7B45 CRC64;

Query Match 36.6%; Score 53; DB 3; Length 807;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWW 13
 ||||| : ||
 Db 624 SSSWLRVSEGW 635

RESULT 10
 Q9IC12 PRELIMINARY; PRT; 3164 AA.

AC Q9IC12;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE POLYPROTEIN.

OS Turnip mosaic virus (strain Japanese) (TuMV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.

QX NCBI_TaxID=12230;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=UK1;
 RA Jenner C.E., Sanchez F., Ponz F., Walsh J.A.;
 RT "The cylindrical inclusion gene of Turnip mosaic potyvirus encodes a
 RT pathogenic determinant to the Brassica resistance gene TuRB01.";
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.

DR EMBL: AF169561; AAF89676.1; -

DR InterPro: IPR001205; -

DR InterPro: IPR001254; -

DR InterPro: IPR001410; -

DR InterPro: IPR001456; -

DR InterPro: IPR001592; -

DR InterPro: IPR001730; -

DR InterPro: IPR002540; -

DR Pfam: PF00270; DEAD; 1.

DR Pfam: PF00680; RNA_dep_RNA_pol; 1.

DR Pfam: PF00767; Poty_coat; 1.

DR Pfam: PF00851; Peptidase_C6; 1.

DR Pfam: PF00863; Peptidase_C4; 1.

DR Pfam: PF01577; Poty_PL; 1.

DR PRINTS; PR00966; NIAPOTYPTASE.

DR SMART; SM00487; DEXDC; 1.

KW ATP-binding; Helicase.

SQ SEQUENCE 3164 AA; 357537 MW; 59D7BAF3734B7991 CRC64;
 Query Match 36.6%; Score 53; DB 14; Length 3164;
 Best Local Similarity 44.4%; Pred. No. 63;
 Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 7 RVFQSWDRNLGRGSSNP 24
 : ||||| : ||| : |
 Db 1261 KTFASWWSHQLSRGTIP 1278

RESULT 11

ID O89177 PRELIMINARY; PRT; 208 AA.

AC O89177;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE ENVELOPE GLYCOPROTEIN (FRAGMENT).

GN ENV.

OS Feline immunodeficiency virus.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11673;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AIC02;

RA Nishimura Y., Goto Y., Hai P., Momoi Y., Endo Y., Mizuno T.,

RA Watarai T., Tsujimoto H., Hasegawa A.;

RT "Genetic heterogeneity of ENV gene of Feline immunodeficiency virus

RT obtained from several districts in Japan.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB010397; BAA31442.1; -

KW Envelope protein.

FT NON_TER 1

FT NON_TER 208

SQ SEQUENCE 208 AA; 24090 MW; CD2AAECE2CEA777B CRC64;

Query Match 35.2%; Score 51; DB 14; Length 208;
 Best Local Similarity 56.2%; Pred. No. 8.3;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWWDRN 16

||| ||| ||| ||

Db 24 QSGSWIRTSSWKORN 39

RESULT 12

O85536 PRELIMINARY; PRT; 224 AA.

ID Q85536;

AC Q85536;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE GP100 (FRAGMENT).

GN ENV.

OS Feline immunodeficiency virus.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11673;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=USILBNY03B;

RX MEDLINE-94187063; PubMed-8139008;

RA Sodora D.L., Shpaer E.G., Kitchell B.E., Dow S.W., Hoover E.A.,

RA Mullins J.I.;

RT "Identification of three feline immunodeficiency virus (FIV) env gene

RT subtypes and comparison of the FIV and human immunodeficiency virus

RT type 1 evolutionary patterns.";

RL J. Virol. 68:2230-2238(1994).

DR EMBL: U02418; AAA18042.1; -

FT NON_TER 1

FT NON_TER 224

SQ SEQUENCE 224 AA; 25902 MW; 05EFAB6FD45A0E4E CRC64;

Query Match 35.2%; Score 51; DB 14; Length 224;
 Best Local Similarity 56.2%; Pred. No. 9;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSSWTRVFQSWWDRN 16

||| ||| ||| ||

Db 41 QSGSWIRTSSWKORN 56

RESULT 13

P87681

ID P87681 PRELIMINARY; PRT; 242 AA.

AC P87681;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)

DE ENV PROTEIN (FRAGMENT).

GN ENV.

OS Feline immunodeficiency virus.

A.Note: var-2

Query Match 10.5%; Score 94.5; DB 2; Length 1729;
Best Local Similarity 21.6%; Pred. No. 6.9; Mismatches 66; Indels 63; Gaps 8;
Matches 42; Conservative 23; Mismatches 66; Indels 63; Gaps 8;
QY 9 PSQEDSSAERGLGSP--AGDGPSSGKHHHQAPGLL-----WDASHQOQPTSSSHH 61
DB 926 PSQEDSSAERGLGSP--AGDGPSSGKHHHQAPGLL-----WDASHQOQPTSSSHH 61
QY 62 GGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRY-----110
DB 983 AGATGLQL-----PGVTVD-----SDPDQTLKRGNIPLNDFLQMFYTLGDYRDICI 1031
QY 111 -----GRLRRMXDEFVDSFKKGLPRPKSAGTATOMROSSWTRVF---151
DB 1032 GGDROIVGTIVITESTGKTKKISKIIEGFLK-----KQTVTSPSPRTSSRTVPHPQT 1086
QY 152 -----QSWMDRN 158
DB 1087 SVEKTPQQTWEAN 1100

RESULT 3
T03166
probable immediate early protein - alcelaphine herpesvirus 1
C:Species: alcelaphine herpesvirus 1
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C:Accession: T03166
R:Essner, A.; Pflanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A:Reference number: Z14840; MUID:97404659
A:Accession: T03166
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1300 <ENS>
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58118.1; PID:g2338034
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 10.3%; Score 93; DB 2; Length 1300;
Best Local Similarity 29.0%; Pred. No. 6.7; Mismatches 56; Indels 14; Gaps 3;
Matches 31; Conservative 6; Mismatches 56; Indels 14; Gaps 3;
QY 5 PEPESEQEDSSAERGLGSP-SPAGDGPSSGKHHHQAPGLLWDASHQOQPTSSSHHG 63
DB 466 PEGEPERPEGEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 521
QY 64 AGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAP 101
DB 522 EGPEGLGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 568

RESULT 4
T42702
hypothetical protein DKFZp434F117.1 - human (fragment)
N:Alternate names: hypothetical protein DKFZp434B239.1
C:Species: Homo sapiens (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C:Accession: T42702; T46502
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: Z22234
A:Accession: T42702
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-834 <AAA>
A:Cross-references: EMBL:AL133028
A:Experimental source: adult testis; clone DKFZp434F117
R:Poustcka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23029
A:Accession: T46502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 213-834 <AA2>
A:Cross-references: EMBL:AL137336
A:Experimental source: adult testis; clone DKFZp434B239
C:Genetics:
A>Note: DKFZp434F117.1; DKFZp434B239.1

Query Match 10.1%; Score 91; DB 2; Length 834;
Best Local Similarity 27.1%; Pred. No. 6.1; Mismatches 49; Conservative 17; Mismatches 51; Indels 64; Gaps 11;
QY 13 EDSSSAERGLGSP---AGDGPSSGKHHHQAPGLLWDASHQOQPTSSSHHGAGAVEI 69
DB 226 EKKHAEAPAGPPRPGDARAGSK-----AKPQESPSSAS--ALAEWASI 272
QY 70 RSR-----HSSYPAGTDEDE-GMGEESP-----FRGRSRAP-----NLWAAQRY---110
DB 273 RSRILKNAESDPRSSERDQLRPGDESTPRGRCDNRGNKTPPVNAKFSIMPWQKFSOG 332
QY 111 GRELRMXDEFVDSFKK-----GLPRPKSAGTATOMROSSWTRVFQSWMDRNLR 161
DB 333 GTETSKQSTE-AESIRKRPMLGPSEETAPQPPAGV-----RELK 372
QY 162 G 162
DB 373 G 373

RESULT 5
A35938
profilaggrin - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 14-Dec-1990 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
A:Accession: A35938
R:Gan, S.Q.; McBride, O.W.; Idler, W.W.; Markova, N.; Steinert, P.M.
Biochemistry 29, 9432-9440, 1990
A:Title: Organization, structure, and polymorphisms of the human profilaggrin gene.
A:Reference number: A35938; MUID:91064347
A:Accession: A35938
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-2248 <GAN>
A:Cross-references: GB:J02929
C:Genetics:
A:Gene: GDB:FLG
A:Cross-references: GDB:119912; OMIM:135940
A:Map position: 1q21-1q21
C:Superfamily: unassigned calmodulin-related proteins; tandem repeat homology
C:Keywords: EF hand; epidermis; polymorphism; tandem repeat
F:246-569/Region: filaggrin repeat
F:570-893/Region: filaggrin repeat
F:1074-1397/Region: filaggrin repeat
F:1573-1896/Region: filaggrin repeat

Query Match 10.1%; Score 91; DB 2; Length 2248;
Best Local Similarity 26.6%; Pred. No. 18; Mismatches 38; Conservative 13; Mismatches 50; Indels 42; Gaps 4;
QY 11 EQEDSSAER-GLGPPSPAGDGPSSGKHHHQAPGLLWDASHQOQPTSSSHHG-----63
DB 152 EQARSAGRHSHHQQASDSSRHSGIGHGQASTAVDSCHRGYRGSGASDNEHSEDSD 211
QY 64 ----AGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSR-----SAP 101
DB 212 SQSVAGORQARSRHQSHQEST-----RGRSGGSGSGSFLYQVSTHQSSES 258
QY 102 PNWAAQRYGRELRLRMXDEFVDS 124

chromogranin A precursor [validated] - bovine
N:Alternate names: pituitary secretory protein I; secretory protein I
N:Contains: chromogranin; pancreastatin
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Aug-2000
C:Accession: A41520; A28033; A24175; A60306; A61114; S15847; S39016; I46008; S38976
R:Racangelo, A.L.; Grimes, M.; Eiden, L.E.
Mol. Endocrinol. 5, 1651-1660, 1991
A:Title: The bovine chromogranin A gene: structural basis for hormone regulation and gene expression
A:Reference number: A41520; MUID:92140395
A:Accession: A41520
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-449 <IAC>
A:Cross-references: GB:S79270; NID:9244423; PIDN:AAE21297.1; PID:9244424
R:Ahm, T.G.; Cohn, D.V.; Gorr, S.U.; Ornstein, D.L.; Kashdan, M.A.; Levine, M.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 5043-5047, 1987
A:Title: Primary structure of bovine pituitary secretory protein I (chromogranin A) deduced from complementary DNA
A:Reference number: A28033; MUID:87260925
A:Accession: A28033
A:Molecule type: mRNA
A:Residues: 1-111, 'T', 113-190, 'Y', 192-253, 'P', 255-378, 'R', 380-449 <AHN>
A:Cross-references: GB:M16971; NID:g163727; PIDN:AAA30765.1; PID:g163728
A:Note: The authors translated the codon CCG for residue 391 as Gln
R:Racangelo, A.; Alfolter, H.U.; Eiden, L.E.; Herbert, E.; Grimes, M.
Nature 323, 82-86, 1986
A:Title: Bovine chromogranin A sequence and distribution of its messenger RNA in endocrine tissues
A:Reference number: A24175; MUID:86311345
A:Accession: A24175
A:Molecule type: mRNA
A:Residues: 1-153, 'PQ', 156-158, 'R', 160-190, 'Y', 192-253, 'P', 255-449 <TA2>
A:Cross-references: GB:X04298; NID:g217; PIDN:CAA27841.1; PID:g218
R:Nakano, I.; Funakoshi, A.; Miyasaka, K.; Ishida, K.; Makk, G.; Angwin, P.; Chang, D.; Regul. Pept. 25, 207-213, 1989
A:Title: Isolation and characterization of bovine pancreastatin.
A:Reference number: A60306; MUID:893331945
A:Accession: A60306
A:Molecule type: protein
A:Residues: 266-312 <NAK>
R:Barbosa, J.A.; Gill, B.M.; Takiyuddin, M.A.; O'Connor, D.T.
Endocrinology 128, 174-190, 1991
A:Title: Chromogranin A: posttranslational modifications in secretory granules.
A:Reference number: A61114; MUID:91099142
A:Accession: A61114
A:Molecule type: protein
A:Residues: 19-34, 'X', 36-38; 97-111; 134-139 <BA2>
R:Watkinson, A.; Joensson, A.C.; Davison, M.; Young, J.; Lee, C.M.; Moore, S.; Dockray, G.
Biochem. J. 276, 471-479, 1991
A:Title: Heterogeneity of chromogranin A-derived peptides in bovine gut, pancreas and adrenal medulla
A:Reference number: S15847; MUID:91264803
A:Accession: S15847
A:Molecule type: protein
A:Residues: 266-310, 'H', 312-318, 'K', 320-331 <WA2>
A:Note: 311-Arg and 319-Glu were also found
R:Watkinson, A.; Rogers, M.; Dockray, G.J.
Biochem. J. 295, 649-654, 1993
A:Title: Post-translational processing of chromogranin A: differential distribution of peptides in secretory granules
A:Reference number: S39016; MUID:94059013
A:Accession: S39016
A:Status: preliminary
A:Molecule type: protein
A:Residues: 303-331 <WA2>
R:Benedum, U.M.; Baeuerle, P.A.; Konecki, D.S.; Frank, R.; Powell, J.; Mallet, J.; Hutterl. EMBO J. 5, 1495-1502, 1986
A:Title: The primary structure of bovine chromogranin A: a representative of a class of secretory granule proteins
A:Reference number: I46008; MUID:86300648
A:Accession: I46008
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-135, 'S', 137-190, 'Y', 192-253, 'P', 255-310, 'H', 312-318, 'K', 320-390, 'Q', 392-444
A:Cross-references: EMBL:X04012; NID:g197; PIDN:CAA27636.1; PID:g198
R:Yoo, S.H.; Ferretti, J.A.
FEBS Lett. 334, 373-377, 1993

A:Title: Nature of the pH-induced conformational changes and exposure of the C-terminus
A:Reference number: S38976; MUID:94063061
A:Accession: S38976
A:Status: preliminary
A:Molecule type: protein
A:Residues: 19-26; 266-272 <YOO>
C:Comment: Chromogranin A is the major protein of bovine chromaggin granules.
C:Comment: Chromogranin activity has been demonstrated from proteolytic fragments of chromogranin A
C:Genetics:
A:Introns: 16/1; 31/3; 63/1; 86/1; 119/1; 266/1; 422/3
C:Superfamily: chromogranin A
C:Keywords: signal sequence #status predicted <SIG>
F:1-18/Domain: signal sequence #status experimental <MAT>
F:19-449/Product: chromogranin A #status predicted <MAT3>
F:142-161/Product: chromogranin A #status predicted <MAT3>
F:266-312/Product: pancreastatin #status experimental <MAT2>
F:35-56/Disulfide bonds: #status predicted

Query Match 9.8%; Score 88.5; DB 1; Length 449;
Best Local Similarity 24.4%; Pred. No. 5;
Matches 39; Conservative 19; Mismatches 57; Indels 45; Gaps 8;

QY 6 EPEPESE---DSSSAERGLGSPAGDPSGSGKHHRRQAPGLLDASHOQEQPTSSHHG 62

Db 138 EYKSEDESDGDRPQASPGLGPGP-----KVEEDNQAPG-----EEEEAPSAH-- 181

QY 63 GAGAVEIRSHSSYPAGTDEDDSGEPSPFRGSRSAAPPNLWAAQRYGRLRRMXD--- 119

Db 182 --PLASLSPKHPGPOAKEDSEGSQGP-----SREKGLSAEQ--GRTEREEEEK 230

QY 120 -EFVDSFKKGLPR-----PKSAGTATQMRQSSW 147

Db 231 WEEAEAREKAVEESPPPTAAFKAPSLGNKETQRAAPGW 270

RESULT 11

hypothetical protein DKFp586G1721.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T43500

R:Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

A:Reference number: 222515

A:Accession: T43500

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-222 <AAA>

A:Cross-references: EMBL:AL133642

A:Experimental source: adult uterus; clone DKFp586G1721

C:Genetics:

A:Note: DKFp586G1721.1

Query Match 9.6%; Score 87; DB 2; Length 222;

Best Local Similarity 27.3%; Pred. No. 3.1;

Matches 41; Conservative 15; Mismatches 56; Indels 38; Gaps 6;

QY 13 EDSSSAERGLGSPAGDPSGSGKHHRRQAPGLLDASHOQEQPTSSHHGAGAVEIRSR 72

Db 77 EDAS-----GGSPSPGTSKS-----DANR-----ASSGGGGGLMEEMNK 111

QY 73 -----HSSYPAGTDEDDSGEP--SPFRG--RSRAPPNLWAAQRYGRLRRMXD 119

Db 112 LLAKRKAASQDKPAEKEDSEQMEDPSTSPGTRAAASQPPNSSEAGKPKWERSNSVE 171

QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTR 149

Db 172 KPVSSILSRTSPVAKSPKSPQSQPHSR 201

RESULT 12

A44067
serine-rich protein hairless - fruit fly (*Drosophila melanogaster*)
N:Alternate names: 109K basic protein H
C:Species: *Drosophila melanogaster*
C:Date: 10-Jun-1993 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999
C:Accession: A44067; A58929; S33412; S24639
R:Bang, A.G.; Posakony, J.W.
Genes Dev. 6, 1752-1769, 1992
A:Title: The *Drosophila* gene *Hairless* encodes a novel basic protein that controls alternative splicing
A:Reference number: A44067; MUID:92387549
A:Accession: A44067
A:Molecule type: DNA
A:Residues: 19-1077 <BAN>
A:Cross-references: GB:M95192; NID:gl57621; PID:gl57622
A:Note: sequence extracted from NCBI backbone (NCBIN:112622, NCBIP:112623)
R:Preiss, A.
submitted to the EMBL Data Library, May 1994
A:Description: *Hairless*, a *Drosophila* gene involved in neural development, encodes a novel serine-rich protein
A:Reference number: A58929
A:Accession: A58929
A:Molecule type: mRNA
A:Residues: 1-1077 <PRE>
A:Cross-references: EMBL:X67239; GB:S49642; NID:g578331; PID:g578332
R:Maier, D.; Stumm, G.; Kuhn, K.; Preiss, A.
Mech. Dev. 38, 143-156, 1992
A:Title: *Hairless*, a *Drosophila* gene involved in neural development, encodes a novel, serine-rich protein
A:Reference number: S33412; MUID:93041287
A:Accession: S33412
A:Molecule type: mRNA
A:Residues: 1-150, 'A', 152-701, 'LL', 704-890, 'R', 892-963, 'RLLP', 968-973, 975-1077 <MAI>
A:Cross-references: EMBL:X67239
C:Genetics:
A:Gene: *FlyBase:H: hairless*
A:Cross-references: *FlyBase:FBgn0001169*

	Query Match	9.6%	Score 86.5;	DB 2;	Length 1077;
	Best Local Similarity	28.9%;	Pred. No. 19;		
	Matches 37;	Conservative 17;	Mismatches 47;	Indels 27;	Gaps 7;
QY	15	SSSAERGLGSPAGDPSG--SGKHHRAQPCLLWDASHQQEQPTSSSHHGAGAVEIRSR	72		
		: :	:		
Db	678	SSSSSG---KKGDHFAATISNVHPQ-----HSMTQPSSSYPRAL----	LTSP	721	
		:	:		
QY	73	HSSYPACTEDDEGMGEPPSPFRGRSRAPPNLWAAQYGRELRMXDFVDSFKKGLP RP	132		
		: : : : : : :			
Db	722	KSPDVSGS-NGGGKSFSTGTAKRFPPIYSAGSPVDYGHSFYR--DPYA-----GAGR P	772		
		:	:		
QY	133	KSAGTATQ 140			
		:: ::			
Db	773	STGSASQ 780			

RESULT 13
S45252
SNF2beta protein - human
C:Species: Homo sapiens (man)
C:Date: 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C:Accession: S45252
R:Chiba, H.; Muramatsu, M.; Nomoto, A.; Kato, H.
Nucleic Acids Res. 22, 1815-1820, 1994
A:Title: Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and Drosophila brm
A:Reference number: S45251; MUID:94268902
A:Accession: S45252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1647 <CHI>
A:Cross-references: GB:D26156; NID:g505087; PIDN:BA05143.1; PID:g505088
C:Superfamily: unassigned bromodomain proteins; bromodomain homology
F:1485-1540/Domain: bromodomain homology <BRO>

Query Match 9.6%; Score 86.5; DB 2; Length 1647;

[illegible]

```

RESULT 14
Tl3049
eyelid - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C:Accession: Tl3049
K:Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z17592
A:Accession: Tl3049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2715 <TRE>
A:Cross-references: EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC06254.1
C:Genetics:
A:Gene: eld
A:Cross-references: FlyBase:FBgn0003013
C:Function:
A:Description: could act as a transcription factor antagonistic to the Wg pathway
C:Keywords: DNA binding

```

[illegible]

RESULT 15
WJMS13
homeotic protein Hox A5 - mouse
N:Alternate names: homeotic protein Hox 1.3; homeotic protein m2
C:Species: Mus musculus (house mouse)
C:date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Sep-1999
C:Accession: S07812; A37051; A38763
R:Ribi, M.; Zink, B.; Kessel, M.; Colberg-Poley, A.M.; Labeit, S.; Lehrach, H.; Gruss
Development 102, 349-359, 1988
A:title: Coding sequence and expression of the homeobox gene Hox 1.3.
A:Reference number: A30340; MUID:88328807

A;Molecule type: mRNA
A;Residues: 1-270 <FMB>
A;Cross-references: EMBL:X16840; NID:g51470; PIDN:CAA34738.1; PID:g51471
R;Odenwald, W.F.; Taylor, C.F.; Palmer-Hill, F.J.; Friedrich Jr., V.; Tani, M.; Lazza
Genes Dev. 1, 482-496, 1987
A;Title: Expression of a homeo domain protein in noncontact-inhibited cultured cells
A;Reference number: A27051; MUID:88056292
A;Accession: A27051
A;Molecule type: DNA
A;Residues: 1-270 <ODE>

QY 121 FVDSFKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAFSQ 168
 |||||
 Db 121 FVDSFKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAFSQ 168

RESULT 2

BAD_MOUSE STANDARD; PRT; 204 AA.
 AC O61337;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
 GN BAD OR BBC6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Thymus;
 RX MEDLINE=95136361; PubMed=7834748;
 RA Yang E., Zhu J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
 RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
 RT promotes cell death.";
 RL Cell 80:285-291(1995).
 CC -!- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE
 CC BINDING TO BCL-X(L) AND BCL-2. THEREBY AFFECTING THE LEVEL
 CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
 CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
 CC -!- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
 CC BAX, MCL-1, AL, OR BCL-X(S).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
 CC -!- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
 CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC
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 CC
 DR EMBL; L37296; AAA64465.1; -;
 DR MGD; MGI:1096330; Bad.
 KW Apoptosis. 138 158 BH1.
 FT DOMAIN 182 199 BH2.
 FT SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 71.5%; Score 645; DB 1; Length 204;
 Best Local Similarity 75.0%; Pred. No. 1.2e-42;
 Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFOIPEFSEQEDSSAERGLGSPAGDGPSSGGRHRAQPCLLWDASHQOQPTSSSH 60
 |||||
 Db 43 MFOIPEFSEQEDASATDGLGFSITEQP---GPY--LAPGLGSLNIHQGRAATNSH 97
 |||||
 QY 61 HGGAGAVEIRSRHSSYPAGTDEDMGEPEFPSPRGRSAPPNLMWAQRYGRELRRMXDE 120
 |||||
 Db 98 HGGAGAMETRSRHSYPAGTDEDMGEELSPPRGRSAPPNLMWAQRYGRELRRMSDE 157
 |||||
 QY 121 FVDSFKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAFSQ 168
 |||||
 Db 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWDRNLGKGSTFSQ 204

RESULT 3

ID CCAA_HUMAN STANDARD; PRT; 2505 AA.

AC O00555; Q92690; Q16290; Q99790; Q99791; Q99792; Q99793; P78510;
 AC P78511;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL
 DE I) (BI).
 GN CACNA1A OR CACNL1A4 OR CACNA4 OR CACNA3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).
 RC TISSUE=Neuron;
 RX MEDLINE=99158614; PubMed=10049321;
 RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
 RA Harpold M.M., Johnson E.C., Williams M.E.;
 RT "Structural elements in domain IV that influence biophysical and
 RT pharmacological properties of human alpha1A-containing
 RT high-voltage-activated calcium channels.";
 RL Biophys. J. 76:1384-1400(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BI-1(VI)), AND VARIANTS FHM.
 RC TISSUE=Cerebellum;
 RX MEDLINE=97053792; PubMed=8898206;
 RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,
 RA Hoffman S.M.G., Lamerding J.E., Mohrenweiser H.W., Bulman D.E.,
 RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
 RA Ferrari M.D., Frants R.R.;
 RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
 RT mutations in the Ca2+ channel gene CACNL1A4.";
 RL Cell 87:543-552(1996).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RX MEDLINE=97141920; PubMed=8988170;
 RA Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
 RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
 RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small
 RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium
 RT channel.";
 RL Nat. Genet. 15:62-69(1997).
 RN [4]
 RP SEQUENCE OF 1693-1807 FROM N.A.
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=95123449; PubMed=7823133;
 RA Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;
 RT "Expression and antibody inhibition of P-type calcium channels in
 RT human small-cell lung carcinoma cells.";
 RL J. Neurosci. 15:274-283(1995).
 RN [5]
 RP SEQUENCE OF 2038-2258 FROM N.A.
 RC TISSUE=Frontal cortex;
 RX MEDLINE=96102310; PubMed=8525433;
 RA Margolis R.L., Breschel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
 RA McInnis M.G., Ross C.A.;
 RT "Characterization of cDNA clones containing CCA trinucleotide repeats
 RT derived from human brain.";
 RL Somat. Cell Mol. Genet. 21:279-284(1995).
 CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A
 CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM
 CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND
 CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-
 CC IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-
 CC GVIA).
 CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT

CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
 CC IN A 1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
 CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
 CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
 CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/Delta
 CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; BI-1(V1)-2, BI-1(V1),
 CC BI-1-GGAG/1A-1 (SHOWN HERE), BI-1(V1)-GGAG, BI-1(V2), BI-1(V2)-
 CC GGAG AND BI-1(V2,V3). ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC. MAINLY FOUND IN CEREBELLUM,
 CC CEREBRAL CORTEX, THALAMUS AND HYPOTHALAMUS. NO EXPRESSION IN
 CC HEART, KIDNEY, LIVER OR MUSCLE. PURKINJE CELLS CONTAIN
 CC PREDOMINANTLY P-TYPE VSCC, THE Q-TYPE BEING A PROMINENT CALCIUM
 CC CURRENT IN CEREBELLAR GRANULE CELLS.
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- POLYMORPHISM: THE POLY-GLN REGION OF CACNA1A IS POLYMORPHIC: 6 TO
 CC 17 REPEATS IN THE NORMAL POPULATION, EXPANDED TO ABOUT 21 TO 30
 CC REPEATS IN SPINOCEREBELLAR ATAXIA 6 (SCA6) PATIENTS. THERE SEEMS
 CC TO BE A CORRELATION BETWEEN THE REPEAT NUMBER AND EARLIER ONSET OF
 CC THE DISORDER.
 CC -1- DISEASE: EXPANSION OF A CAG REPEAT IN THE CODING REGION OF CACNA1A
 CC IS THE CAUSE OF ONE FORM OF SPINOCEREBELLAR ATAXIA 6 (SCA6), AN
 CC AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY SLOWLY PROGRESSIVE
 CC CEREBELLAR ATAXIA OF THE LIMBS AND GAIT, DYSARTHRIA, NYSTAGMUS,
 CC AND MILD VIBRATORY AND PROPRIOCEPTIVE SENSORY LOSS. THESE SYMPTOMS
 CC ARE PROBABLY EXPLAINED BY SEVERE LOSS OF CEREBELLAR PURKINJE
 CC CELLS.
 CC -1- DISEASE: DEFECTS IN CACNA1A ARE THE CAUSE OF FAMILIAL HEMIPLEGIC
 CC MIGRAINE (FHM), ALSO KNOWN AS MIGRAINE FAMILIAL HEMIPLEGIC 1
 CC (NHP1), EPISODIC ATAXIA TYPE 2 (EA-2), ACETAZOLAMIDE-RESPONSIVE
 CC HEREDITARY PAROXYSMAL CEREBELLAR ATAXIA (APCA), AND POSSIBLY OTHER
 CC COMMON TYPES OF MIGRAINES. FHM, A RARE AUTOSOMAL DOMINANT SUBTYPE
 CC OF MIGRAINE WITH AURA, IS ASSOCIATED WITH ICTAL HEMIPARESIS AND,
 CC IN SOME FAMILIES, PROGRESSIVE CEREBELLAR ATROPHY. EA-2 IS ANOTHER
 CC AUTOSOMAL DOMINANT PAROXYSMAL CEREBRAL DISEASE, CHARACTERIZED BY
 CC ACETAZOLAMIDE-RESPONSIVE ATTACKS OF CEREBELLAR ATAXIA AND
 CC MIGRAINE-LIKE SYMPTOMS, INTERICTAL NYSTAGMUS, AND CEREBELLAR
 CC ATROPHY.
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF004884; AAB61613.1; -;
 CC EMBL; AF004883; AAB61612.1; -;
 CC EMBL; X9897; CAA68172.1; -;
 CC EMBL; Z80114; -; NOT_ANNOTATED_CDS.
 CC EMBL; Z80115; -; NOT_ANNOTATED_CDS.
 CC EMBL; U79666; AAB64179.1; -;
 CC EMBL; U79663; AAB49674.1; ALT_INIT.
 CC EMBL; U79664; AAB49675.1; ALT_INIT.
 CC EMBL; U79665; AAB49676.1; ALT_INIT.
 CC EMBL; U79667; AAB49677.1; ALT_INIT.
 CC EMBL; U79668; AAB49678.1; ALT_INIT.
 CC EMBL; S76537; AAB33068.1; -;
 CC EMBL; U06702; -; NOT_ANNOTATED_CDS.
 CC MIM; 601011; -;
 CC MIM; 183086; -;
 CC MIM; 141500; -;
 CC InterPro; IPR000636; -;
 CC InterPro; IPR002077; -;
 CC Pfam; PF00520; ion_trans; 4.

DR PRINTS; PR00167; CACHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Cation channel; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation; Alternative splicing; Polymorphism;
 KW Disease mutation; triplet repeat expansion.
 FT REPEAT 85 363 I.
 FT REPEAT 473 717 II.
 FT REPEAT 1231 1514 III.
 FT REPEAT 1551 1814 IV.
 FT DOMAIN 1 98 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 99 117 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 118 135 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 136 155 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 156 167 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 168 185 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 186 190 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 191 209 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 210 228 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 229 248 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 249 335 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 336 360 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 361 487 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 488 506 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 507 521 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 522 541 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 542 549 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 550 568 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 569 578 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 579 597 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 598 616 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 617 636 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 637 689 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 690 714 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 715 1242 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1243 1261 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1262 1277 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1278 1297 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1298 1309 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1310 1328 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1329 1339 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1340 1358 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1359 1377 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1378 1397 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1398 1484 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1485 1509 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1510 1564 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1565 1593 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1594 1598 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1599 1618 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1619 1626 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 1627 1645 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1646 1652 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 1653 1671 S4 OF REPEAT IV (POTENTIAL).
 Query Match 10.6%; Score 96; DB 1; Length 2505;
 Best Local Similarity 23.5%; Pred. No. 6.9;
 Matches 48; Conservative 22; Mismatches 54; Indels 80; Gaps 11;
 Qy 5 PEPFPEQED-----SSSAERGLGSP---AGDGGSGSKHHRQAP----- 42
 Db 2313 PQQQQQQQQQQAVARPGRAATGPRYPGTAEPGLADRPPTGGHSSGSRPERRVPG 2372
 Qy 43 -----GLLWDAS--HQEQPTSSSHHGAGAVEIRSRHSSYPACTEDDE--- 84
 Db 2373 PARESPPRACHRGAGRWASGPHVSEGGPPGRHHG-----YRGSDYDEADG 2419
 Qy 85 ---GMGEJ-----PSPFR-----GRS-----RSAPPNLWAAQRYGRLRRMXDEFV 122
 Db 2420 PGSGGGEAMAGAYDAPPPVRHASSGATGRSPRTFRASGPACASPSRHG---RRLPNGY 2476
 Qy 123 DSFKKGLPRPKSAGTATQMROSSS 146
 Db 2477 PA--HGLARPRGPGSRKGLHEPYS 2498

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RESULT 4
ID CYAA_NEUCR STANDARD; PRT; 2300 AA.
AC Q01611;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
DE CYCLASE).
GN CR-1 OR NAC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92000795; PubMed=1680356;
RA Kore-Eda S., Murayama T., Uno I.;
RT "Isolation and characterization of the adenylate cyclase structural
RT gene of Neurospora crassa."
RL Jpn. J. Genet. 66:317-334(1991).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CC CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL; D00909; BAA00755.1; -
DR InterPro; IPR001611; -
DR InterPro; IPR001932; -
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PR00019; LEURICHRPT.
DR PROSITE; PS0125; GUANYLATE CYCLASES 2; 1.
KW Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT REPEAT 867 890
FT REPEAT 892 914
FT REPEAT 915 938
FT REPEAT 938 961
FT REPEAT 962 986
FT REPEAT 988 1008
FT REPEAT 1009 1031
FT REPEAT 1033 1055
FT REPEAT 1056 1079
FT REPEAT 1081 1097
FT REPEAT 1098 1120
FT REPEAT 1122 1142
FT REPEAT 1143 1165
FT REPEAT 1166 1188
FT REPEAT 1189 1211
FT REPEAT 1213 1234
FT REPEAT 1349 1369
FT REPEAT 1373 1396
FT REPEAT 1398 1420
FT REPEAT 1422 1445
FT REPEAT 1447 1469
FT REPEAT 1474 1497
FT REPEAT 1513 1538
FT REPEAT 1564 1829
FT DOMAIN 1830 2300
FT DOMAIN 49 52
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FT DOMAIN 204 221 POLY-GLN.
SQ SEQUENCE 2300 AA; 254752 MW; 52E79B90E6B17A7B CRC64;

Query Match 10.0%; Score 90.5; DB 1; Length 2300;
Best Local Similarity 23.7%; Pred. No. 17;
Matches 50; Conservative 23; Mismatches 75; Indels 63; Gaps 11;

QY 17 SAERGLGSPAGDPSGKHKHR---QAPGLLDASHOQEQPTSSSHH-----GGAGAV 67
DB 343 SSEISL-PPSHSGPMSTGKHSYSLPGS--GSHRDRNYSNATDHPSTFGSVSTV 399

QY 68 EIKSRHS-----YPA-----GTEDDEGMGEPE-----SPFRGR---SRSA 100
DB 400 GGRDROASVPSPRPRTVPVPAPEVVPFLYQEAADDIARYGEAPVRTSLTGPDRLDYIDSSQN 459

QY 101 PPNLWAAQRYGREL-----RRMXDEFVDSFKKGLPRPKSAGT-----AT 139
DB 460 PRTSSARSAGHSIVHLPGHHKHNKSDPRALKPSRLSREDSAAFSARDFRNGSSMMGT 519

QY 140 QMRQSS---SWTRVFOSWDRNLGRGSSAPS 167
DB 520 RSRAQSPAPSWTGTSGRLKANSISDGTSSPA 550

RESULT 5
CCAB_HUMAN
ID CCAB_HUMAN STANDARD; PRT; 2339 AA.
AC Q00975;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
DE III) (BIII).
GN CACNA1B OR CACNLIA5 OR CACHS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2)...
RX TISSUE=Brain;
RX MEDLINE=92335886; PubMed=1321501;
RA Williams M.E., Brust P.F., Feldman D.H., Patthi S., Simerson S.,
RA Maroufi A., McCue A.F., Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of an omega-conotoxin-sensitive
RT human N-type calcium channel."
RL Science 257:389-395(1992).
RN [2]
RP SEQUENCE OF 1-94 FROM N.A.
RC TISSUE=Lung fibroblast;
RA Kim D.S., Jung H.H., Park S.H., Chin H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
CC GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
CC BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC BY OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOXIN-
CC IIIA (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO
CC DIHYDROPYRIDINES (DHP). AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
CC DIRECTED MIGRATION OF IMMATURE NEURONS.
CC -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
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RX MEDLINE=92140395; PubMed=1779968;
 RA Tacangelo A.L., Grimes M., Eiden L.E.;
 RT "The bovine chromogranin A gene: structural basis for hormone
 RL regulation and generation of biologically active peptides.";
 RL Mol. Endocrinol. 5:1651-1660(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86300648; PubMed=3755681;
 RA Benedum U.M., Baeuerle P.A., Konecki D.S., Frank R., Powell J.,
 RA Mallet J., Huttner W.B.;
 RT "The primary structure of bovine chromogranin A: a representative of
 RT a class of acidic secretory proteins common to a variety of
 RT peptidergic cells.";
 RL EMBO J. 5:1495-1502(1986).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86311345; PubMed=3018587;
 RA Tacangelo A., Affolter H.-U., Eiden L.E., Herbert E., Grimes M.;
 RT "Bovine chromogranin A sequence and distribution of its messenger RNA
 RT in endocrine tissues.";
 RL Nature 323:82-86(1986).
 RN [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87260925; PubMed=3474638;
 RA Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
 RA Levine M.A.;
 RT "Primary structure of bovine pituitary secretory protein I
 RT (chromogranin A) deduced from the cDNA sequence";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:5043-5047(1987).
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97228583; PubMed=9074643;
 RA Kang Y.K., Yoo S.H.;
 RT "Identification of the secretory vesicle membrane binding region of
 RT chromogranin A.";
 RL FEBS Lett. 404:87-90(1997).
 RN [6]
 RN SEQUENCE OF 19-45, AND CALCIUM-BINDING.
 RX MEDLINE=90354431; PubMed=2387861;
 RA Yoo S.H., Albanesi J.P.;
 RT "Ca2(+)-induced conformational change and aggregation of chromogranin
 RT A.";
 RL J. Biol. Chem. 265:14414-14421(1990).
 RN [7]
 RN SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
 RX MEDLINE=91142185; PubMed=1996343;
 RA Galindo E., Rill A., Bader M.-F., Aunis D.;
 RT "Chromostatin, a 20-amino acid peptide derived from chromogranin A,
 RT inhibits chromaffin cell secretion.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:1426-1430(1991).
 RN [8]
 RN ERRATUM.
 RA Galindo E., Rill A., Bader M.-F., Aunis D.;
 RL Proc. Natl. Acad. Sci. U.S.A. 91:832-832(1994).
 RN [9]
 RN SEQUENCE OF 266-312.
 RX MEDLINE=89331945; PubMed=2756155;
 RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Angwin P.,
 RA Chang D., Tatemoto K.;
 RT "Isolation and characterization of bovine pancreastatin.";
 RL Regul. Pept. 25:207-213(1989).
 RN [10]
 RN SEQUENCE OF 191-212 (CHROMACIN).
 RC TISSUE=Chromaffin granules;
 RX MEDLINE=97067080; PubMed=8910482;
 RA Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,
 RA van Dorsselaer A., Aunis D., Metz-Boutigue M.-H.;
 RT "Antibacterial activity of glycosylated and phosphorylated
 RT chromogranin A-derived peptide 173-194 from bovine adrenal medullary
 RT chromaffin granules.";
 RL J. Biol. Chem. 271:28533-28540(1996).
 RN [11]
 RN CHARACTERIZATION OF CATESTATIN.
 RX MEDLINE=97439785; PubMed=9294131;
 RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,
 RA Gill B.M., Parmer R.J.;
 RT "Novel autocrine feedback control of catecholamine release. A discrete
 RT chromogranin A fragment is a noncompetitive nicotinic cholinergic
 RT antagonist.";
 RL J. Clin. Invest. 100:1623-1633(1997).
 RN [12]
 RN CHARACTERIZATION OF CATESTATIN.
 RX MEDLINE=99000113; PubMed=9786174;
 RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
 RT "Mechanism of cardiovascular actions of the chromogranin A fragment
 RT catestatin in vivo.";
 RL Peptides 19:1241-1248(1998).
 RN [13]
 RN 3D-STRUCTURE MODELING OF CATESTATIN.
 RX MEDLINE=99025667; PubMed=9809795;
 RA Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
 RA Khan I., Parmer R.J., O'Connor D.T.;
 RT "Mechanism of action of chromogranin A on catecholamine release:
 RT molecular modeling of the catestatin region reveals a beta-
 RT strand/loop/beta-strand structure secured by hydrophobic interactions
 RT and predictive of activity.";
 RL Regul. Pept. 77:43-53(1998).
 RN [14]
 RN CHARACTERIZATION OF VASOSTATIN-1.
 RX MEDLINE=20219105; PubMed=10753865;
 RA Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
 RA Aunis D., Metz-Boutigue M.-H.;
 RT "Antibacterial and antifungal activities of vasostatin-1, the N-
 RT terminal fragment of chromogranin A";
 RL J. Biol. Chem. 275:10745-10753(2000).
 RN [15]
 RN CARBOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
 RX MEDLINE=99459228; PubMed=10527498;
 RA Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
 RT "Chromogranin A from bovine adrenal medulla: molecular
 RT characterization of glycosylations, phosphorylations, and sequence
 RT heterogeneities by mass spectrometry.";
 RL Anal. Biochem. 274:69-80(1999).
 CC -!- FUNCTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN
 CC RELEASE FROM THE PANCREAS.
 CC -!- FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE
 CC FROM CHROMAFFIN CELLS.
 CC -!- FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
 CC LUTEUS.
 CC -!- FUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM
 CC CHROMAFFIN CELLS AND NORADRENERGIC ANTAGONIST.
 CC -!- FUNCTION: VASOSTATIN-1 HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-
 CC POSITIVE BACTERIA M.LUTEUS, B.MEGATERIUM. NOT ACTIVE AGAINST GRAM-
 CC POSITIVE BACTERIA B.CEREUS, B.SUBTILIS, S.PYROGENES, M.FORTUITUM,
 CC S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-NEGATIVE BACTERIA
 CC E.COLI, E.CLOACAE, S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURIGINOSA.
 CC POSSESSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.FUMIGATUS,
 CC A.BRASSICOLA, N.HEMATOCOCCA, F.CULMORUM AND F.OXYSPORUM AND
 CC AGAINST S.CEREVISIAE AND C.ALBICANS YEAST. INACTIVE AGAINST
 CC T.MENTAGROPHYTES.
 CC -!- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
 CC GRANULES.
 CC -!- MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.
 CC -!- MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
 CC -!- SIMILARITY: BELONGS TO THE CHROMOGANIN / SECRETORANIN PROTEIN
 CC FAMILY.
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FT DOMAIN 1571 1584 POLY-GLU.
SQ SEQUENCE 1647 AA; 184585 MW; 7B785E7953277F1D CRC64;

Query Match 9.6%; Score 86.5; DB 1; Length 1647;
Best Local Similarity 29.8%; Pred. No. 24;
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;

QY 9 PSEQEDSSSAERGLGPGSPAGDGGSGGKHH---RQAP-GLLWDASHQEQPTSSSHHGA 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 30 PSGPSPGSAHSMGPFSP---GPFSAG--HPITQPGGYPQDNMHQMHKPMESMHEKGM 84
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 65 GAVEIRSHRSYSPAGTDEDDGMEGPEEPFGRGRSRAPPNLWAAQ 108
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 SDDPRYNQMGMRSGGHAGMGPPPPPMQDHSOGYPSPLGGSE 128
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT. 9
HXA5_MOUSE STANDARD; PRT; 270 AA.
AC P09021;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE HOMEBOX PROTEIN HOX-A5 (HOX-1.3) (M2).
GN HOXA5 OR HOXA-5 OR HOX-1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056292; PubMed=2890554;
RA Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr.,
RA Tani M., Lazzarini R.A.;
RT "Expression of a homeo domain protein in noncontact-inhibited
RT cultured cells and postmitotic neurons.";
RL Genes Dev. 1:482-496(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88328807; PubMed=2901335;
RA Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labelt S.,
RA Lehrach H., Gruss P.;
RT "Coding sequence and expression of the homeobox gene Hox 1.3.";
RL Development 102:349-359(1988).
RN [3]
RP DNA-BINDING SPECIFICITY.
RX MEDLINE=89232713; PubMed=2565857;
RA Odenwald W.F., Garbern J., Arnheiter H., Tournier-Lasserre E.,
RA Lazzarini R.A.;
RT "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
RT phosphoprotein.";
RL Genes Dev. 3:158-172(1989).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=96205869; PubMed=8635464;
RA Zhao J.J., Lazzarini R.A., Pick L.;
RT "Functional dissection of the mouse Hox-a5 gene.";
RL EMBO J. 15:1313-1322(1996).
RN [5]
RP FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
RN A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
RN SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
RN ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
RN 5'-CYNNATTA[GTG]-3'.
RN [6]
RP SUBCELLULAR LOCATION: NUCLEAR.
RN [7]
RP DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
RN KIDNEY.
RN [8]
RP SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
RN [9]
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```
CC EMBL; M36604; AAA37838.1; -
CC EMBL; Y00208; CAA68364.1; -
CC EMBL; X16840; CAA34738.1; -
CC EMBL; M28021; AAA37837.1; -
CC PIR; S07812; WJMS13.
CC HSSP; P02833; 1SAN.
CC TRANSFAC; T00377; -
CC MGD; MGI:96177; Hoxa5.
CC InterPro; IPR001356; -
CC InterPro; IPR001827; -
CC Pfam; PF00046; homeobox.1.
CC PRINTS; PR00024; HOMEOBOX.
CC PRINTS; PR00025; ANTENNAPEDIA.
CC PROSITE; PS00027; HOMEOBOX.1; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; 1.
CC PROSITE; PS00071; HOMEOBOX.2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT DOMAIN 176 181 ANTP-TYPE HEXAPEPTIDE.
FT DNA_BIND 195 254 HOMEOBOX.
SQ SEQUENCE 270 AA; 29237 MW; DC4BDDA8FE62766E CRC64;

Query Match 9.58; Score 86; DB 1; Length 270;
Best Local Similarity 25.88; Pred. No. 4;
Matches 55; Conservative 13; Mismatches 63; Indels 82; Gaps 11;

Qy 10 SEQ-EDSSABERG-----LGPSPAGDGPSPGSGKHHRQ-----APGLLDASHQ 51
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 SEQFRDSASMHSGRYGYNGMDLSVGRSGSGHFGSGERARSYAAGASAP-----AEPR 85
   ||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 52 QEQPTSS-----SHGG-----AGAVEIRSR----- 72
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 YSQPATSTHPPDPLPCSAVAPSPGSDSHRGKNSLGNSSGASANAGSTHSSREGVGT 145
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 73 ----HSSYPACTDEGMEEPSPFRGSRAPPNLMAQAAGYGRRLRMXDEEVDSPFKG 128
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 ASAAEDAPASSE-QAGAQSESP-----APPAQPIYPMWKLHSHDNI-----G 191
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 129 LPRPKSACTATQMRQSSSWTFVQSWDNRNLGR 161
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 192 GPEGKRARTATRYOTLELEKEFH--FNRYLTR 222
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
ID SGL_BOVIN STANDARD; PRT; 646 AA.
AC P23389; 002707;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
DE PEPTIDE; SECRETOLYTIN].
GN CHGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUP-Adrenal Chromaffin;
RA MEDLINE=91223091; PubMed=2025642;
RX Bauer J.W., Fischer-Colbrie R.;
"Primary structure of bovine chromogranin B deduced from cDNA
sequence.";
RL Biochim. Biophys. Acta 1089:124-126(1991).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC TISSUP-Adrenal medulla;
RX MEDLINE=97282588; PubMed=9136897;
RA Yoo S.H., Kang Y.K.;
RT "Identification of the secretory vesicle membrane binding region of
chromogranin B.";
RL FEBS Lett. 406:259-262(1997).
[3]
RP SEQUENCE OF 21-646 FROM N.A.
RC TISSUP-Adrenal medulla;
RA Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J.,
Thomas G., Civelli O., Viveros O.H.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 634-646.
RC TISSUP-Adrenal chromaffin;
RX MEDLINE=95262699; PubMed=7744058;
RA Strub J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
van Dorselaer A., Aunis D., Metz-Boutigue M.-H.;
RT "Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolytin, the endogenous C-terminal fragment of
residues 614-626 with antibacterial activity.";
RL Eur. J. Biochem. 229:356-368(1995).
[5]
RP CHARACTERIZATION OF SECRETOLYTIN.
RX MEDLINE=96184581; PubMed=8603705;
RA Strub J.M., Hubert P., Nullans G., Aunis D., Metz-Boutique M.-H.;
RT "Antibacterial activity of secretolytin, a chromogranin B-derived
peptide (614-626), is correlated with peptide structure.";
RL FEBS Lett. 379:273-278(1996).
CC -1- FUNCTION: SECRETOGRANIN I IS A NEUROENDOCRINE SECRETORY GRANULE
PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE
PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS
SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.
CC -1- FUNCTION: SECRETOLYTIN HAS ANTI-BACTERIAL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
GRANULES.
CC -1- PTM: O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
FAMILY.
CC -----
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CC EMBL; X55027; CAA38846.1; -
CC EMBL; U88551; AAC48720.1; -
CC EMBL; X55489; CAA39109.1; -
CC PIR; S15901; S15901.
CC InterPro; IPR001819; -
CC InterPro; IPR001990; -
CC Pfam; PF01271; Granin; 1.
CC PRINTS; PR00659; CHROMOGRANIN.
CC PROSITE; PS00422; GRANINS.1; 1.
CC PROSITE; PS00423; GRANINS.2; 1.
CC Sulfatation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT CHAIN 21 646 SECRETOGRANIN I.
FT PEPTIDE 418 484 GAWK PEPTIDE.
FT PEPTIDE 634 646 SECRETOLYTIN.
FT DISULFID 36 57 BY SIMILARITY.
FT MOD_RES 158 158 SULFATATION (POTENTIAL).
FT MOD_RES 315 315 SULFATATION (BY SIMILARITY).
FT CONFLICT 64 64 N -> S (IN REF. 1).
FT CONFLICT 70 70 N -> D (IN REF. 2).
FT CONFLICT 93 98 SEAPGL -> FRSPRAS (IN REF. 3).
FT CONFLICT 181 181 T -> M (IN REF. 2).
FT CONFLICT 261 261 H -> R (IN REF. 2).
FT CONFLICT 386 386 P -> R (IN REF. 2).
FT CONFLICT 481 481 H -> L (IN REF. 3).
```


QY 82 DDEGMGEPSRGRSRAPPNLAQAQRYGRELRRMXDFVDFKKGKGLPRPKSAGTATOM 141
Db 151 EDAPASSEQASQSESPAPPAQPIYPMWKLHSHDNI-----GGPEGKARTAYTR 204
QY 142 ROSSWTRVFQSWDRNLGR 161
Db 205 YQTELEKEFH--FNRYLFR 222

RESULT 15
VASP_HUMAN STANDARD; PRT; 380 AA.
AC P50552; Q93035;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).
GN VASP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95129547; PubMed=7828592;
RA Haffner C., Jarchau T., Reinhard M., Hoppe J., Lohmann S.M.,
RA Walter U.;
RT "Cloning of the VASP (vasodilator-stimulated phosphoprotein) genes in
RT human and mouse: structure, sequence, and chromosomal localization.";
RL Genomics 36:227-233(1996).
RN [2]
RL EMBO J. 14:19-27(1995).
RN [3]
RP SEQUENCE OF 151-160; 235-244 AND 267-282, AND PHOSPHORYLATION SITES.
RX MEDLINE=94237860; PubMed=8182057;
RA Butt E., Abel K., Krieger M., Palm D., Hoppe V., Hoppe J., Walter U.;
RT "CAMP- and CGMP-dependent protein kinase phosphorylation sites of the
RT focal adhesion vasodilator-stimulated phosphoprotein (VASP) in vitro
RT and in intact human platelets";
RL J. Biol. Chem. 269:14509-14517(1994).
RN [4]
RP BINDING TO PROFILIN.
RX MEDLINE=9525215; PubMed=7737110;
RA Reinhard M., Giehl K., Abel K., Haffner C., Jarchau T., Hoppe V.,
RA Jockusch B.M., Walter U.;
RT "The proline-rich focal adhesion and microfilament protein VASP is a
RT ligand for profilins";
RL EMBO J. 14:1583-1589(1995).
CC -!- FUNCTION: ACTIN- AND PROFILIN-BINDING MICROFILAMENT-ASSOCIATED
CC PROTEIN. MAY ACT IN CONCERT WITH PROFILIN TO CONVEY SIGNAL
CC TRANSDUCTION TO ACTIN FILAMENT PRODUCTION.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: FOCAL ADHESIONS.
CC -!- PTM: MAJOR SUBSTRATE FOR CAMP-DEPENDENT (CAPK) AND CGMP-DEPENDENT
CC PROTEIN KINASE (CGPK) IN PLATELETS.
CC -----
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CC -----
DR EMBL; 246389; CAA86523.1; -.
DR EMBL; X98534; CAA67147.2; -.

DR EMBL; X98533; CAA67147.2; JOINED.
DR MIM; 601703; -.
DR InterPro; IPR001960; -.
DR Pfam; PF00568; WHI; 1.
KW Phosphorylation; Actin-binding.
FT DOMAIN 118 122 POLY-PRO.
FT DOMAIN 170 186 POLY-PRO.
FT DOMAIN 215 222 POLY-GLY.
FT DOMAIN 259 262 POLY-GLY.
FT DOMAIN 322 325 POLY-SER.
FT MOD_RES 157 157 PHOSPHORYLATION (BY CAPK AND CGPK).
FT MOD_RES 239 239 PHOSPHORYLATION (BY CAPK AND CGPK).
FT MOD_RES 278 278 PHOSPHORYLATION (BY CAPK AND CGPK).
SQ SEQUENCE 380 AA; 39830 MW; 17634B8134DEBF59 CRC64;

Query Match 9.3%; Score 84; DB 1; Length 380;
Best Local Similarity 24.9%; Pred. No. 8.1;
Matches 43; Conservative 18; Mismatches 52; Indels 60; Gaps 10;

QY 17 SAERGLG-----PSPAGDGPSSGSKHHRQAPGL-----LWDASHQEQ---PTS- 57
Db 195 AAHGAGGGPPPPAPPAPAAQGGPGGG---AGAPGLAAAIAGAKLRKVKQEEASGGPTAP 251
QY 58 ---SSHHGGAGAVE-----IRSRHSYPAG---TEDDEGMGEPS-----PFR 94
Db 252 KAESGRSGGGGLMEEMNMLARRKATQVGEKTPKDESANQEEPEARVPAQSESVRRPWE 311
QY 95 GRSRAP-----PMLAAQRYGRELRRMXDFVDFKKGKGLPRPK 133
Db 312 KNSTTLPRMKSSSVTSETQCTPSSSDYS-DLQRVKQELLEEVKKELQVKV 363

Search completed: October 9, 2001, 16:03:43
Job time: 308 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:15 ; Search time 35.13 seconds
(without alignments)
632.714 Million cell updates/sec

Title: 09-580523-la
Perfect score: 902
Sequence: 1 MFQIPFEPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	99.9	168	014803	014803 homo sapien
2	632.5	70.1	205	11 035147	035147 rattus norv
3	632.5	70.1	205	11 070256	070256 rattus norv
4	442	49.0	220	11 09JHX1	09JHX1 rattus norv
5	203.5	22.6	95	13 0919N2	0919N2 brachydania
6	100	11.1	608	14 09QSK9	09QSK9 herpesvirus
7	98.5	10.9	569	13 09DF20	09DF20 brachydania
8	98	10.9	272	4 09NS37	09NS37 homo sapien
9	98	10.9	355	2 09RDL8	09RDL8 streptomyc
10	96.5	10.7	867	10 09FVZ6	09FVZ6 oryza sativ
11	95.5	10.6	980	4 095387	095387 homo sapien
12	95.5	10.6	2506	4 09NS88	09NS88 homo sapien
13	94.5	10.5	923	5 09NKN4	09NKN4 leishmania
14	94.5	10.5	1729	5 025734	025734 plasmodium
15	93.5	10.4	549	4 09H0B9	09H0B9 homo sapien
16	93.5	10.4	1203	4 09UPQ9	09UPQ9 homo sapien
17	93.5	10.4	1398	11 009000	009000 mus musculu
18	93	10.3	1146	5 09N809	09N809 trypanosoma
19	93	10.3	1300	14 036421	036421 alcelaphine

20	92.5	10.3	1082	11 09EPU2	09EPU2 rattus norv
21	92	10.2	2472	4 09NS89	09NS89 homo sapien
22	91	10.1	622	4 09NTE2	09NTE2 homo sapien
23	91	10.1	670	5 09NEL2	09NEL2 caenorhabdi
24	91	10.1	701	4 09NTP8	09NTP8 homo sapien
25	91	10.1	803	4 09ULK9	09ULK9 homo sapien
26	91	10.1	990	4 015206	015206 homo sapien
27	91	10.1	1218	4 005331	005331 homo sapien
28	90	10.0	414	11 09ERU8	09ERU8 mus musculu
29	90	10.0	474	5 09VA96	09VA96 drosophila
30	89.5	9.9	393	11 008719	008719 rattus norv
31	89.5	9.9	393	11 070429	070429 mus musculu
32	89.5	9.9	947	10 09LWJ9	09LWJ9 oryza sativ
33	89	9.9	903	4 09UPX1	09UPX1 homo sapien
34	88.5	9.8	336	14 098321	098321 molluscum c
35	88.5	9.8	809	5 09NAN8	09NAN8 caenorhabdi
36	88	9.8	362	4 095884	095884 homo sapien
37	88	9.8	416	4 09UI08	09UI08 homo sapien
38	88	9.8	418	4 09UIC2	09UIC2 homo sapien
39	88	9.8	462	6 097643	097643 lama glama
40	88	9.8	735	11 09JIG4	09JIG4 mus musculu
41	88	9.8	956	4 09UQ39	09UQ39 homo sapien
42	88	9.8	1262	4 09UQ40	09UQ40 homo sapien
43	88	9.8	2296	4 09UHA8	09UHA8 homo sapien
44	88	9.8	2752	4 09UQ35	09UQ35 homo sapien
45	87.5	9.7	510	5 09VAI8	09VAI8 drosophila

ALIGNMENTS

RESULT 1

014803	PRELIMINARY;	PRT;	168 AA.
ID 014803			
AC 014803			
DT 01-JAN-1998	(TRENBLREL. 05, Created)		
DT 01-JAN-1998	(TRENBLREL. 05, Last sequence update)		
DT 01-NOV-1998	(TRENBLREL. 08, Last annotation update)		
DE BCL-X/BCL-2	BINDING PROTEIN (FRAGMENT).		
GN BAD.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=97083574; PubMed=8929532;			
RA Wang H.G., Rapp U.R., Reed J.C.;			
RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria."			
RL Cell 87:629-638(1996).			
RN [2]			
RP SEQUENCE FROM N.A.			
RA Takayama S., Reed J.C.;			
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN [3]			
RP SEQUENCE FROM N.A.			
RA Ottilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,			
RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;			
RL J. Biol. Chem. 0:0-0(1997).			
DR EMBL; AF021792; AAB72092.1;			
DR EMBL; AF031523; AAB88124.1;			
FT NON_TER			
SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;			

Query Match 99.9%; Score 901; DB 4; Length 168;
Best Local Similarity 99.4%; Pred. No. 2.2e-76;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRRQAPGLLWDASHOQEQPTSSSH	60
Db	1	MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRRQAPGLLWDASHOQEQPTSSSH	60

QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMXDE 120
Db HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
RESULT 2
Q35147
ID O35147 PRELIMINARY; PRT; 205 AA.
AC O35147;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER.
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
DR EMBL; AF003523; AAC53374.1; -.
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;

Query Match 70.1%; Score 632.5; DB 11; Length 205;
Best Local Similarity 74.6%; Pred. No. 2.3e-51;
Matches 126; Conservative 11; Mismatches 25; Indels 7; Gaps 4;
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59
Db MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59
QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMXD 119
Db HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMSD 157
QY 120 EFVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db EFVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 205

RESULT 3
O70256
ID O70256 PRELIMINARY; PRT; 205 AA.
AC O70256;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
ALPHA).
GN BAD OR BAD-ALPHA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98194755; PubMed=95351132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator Bad in
the rat brain";
RL Neurosci. Lett. 243:137-140(1998).

RNA SEQUENCE FROM N.A.
RA Hammer S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF031227; AAC15100.1; -.
DR EMBL; AF279911; AAF91427.1; -.
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 70.1%; Score 632.5; DB 11; Length 205;
Best Local Similarity 74.6%; Pred. No. 2.3e-51;
Matches 126; Conservative 11; Mismatches 25; Indels 7; Gaps 4;
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59
Db MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59
QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMXD 119
Db HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMSD 157
QY 120 EFVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db EFVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 205

RESULT 4
Q9JHX1
ID Q9JHX1 PRELIMINARY; PRT; 220 AA.
AC Q9JHX1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.
GN BAD-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hammer S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF279911; AAF91428.1; -.
SQ SEQUENCE 220 AA; 24278 MW; E27BCDD7C969E90F CRC64;

Query Match 49.0%; Score 442; DB 11; Length 220;
Best Local Similarity 71.7%; Pred. No. 1.2e-33;
Matches 91; Conservative 8; Mismatches 22; Indels 6; Gaps 3;
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 59
Db MFOIPEFEPSEQDSSAERGLGSPAGDPGSGGKHHRQAPGLLWDASHQOE-QPTSSS 97
QY 60 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMXD 119
Db HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFPRGRSRAPPNLWAAQRYGRELRRMSD 157
QY 120 EFVDSFK 126
Db EFVDSFK 164
RESULT 5
Q9I9N2
ID Q9I9N2 PRELIMINARY; PRT; 95 AA.
AC Q9I9N2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)


```
*
Db 869 PHVSEGGPPRRHG-----YRGSYDEADPGSGGEEAMAGAYDAPPVVR 915
QY 95 -----GRS-----RSAPPNLWAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQ 143
Db 916 HASSGATGRSPRTPRASGPACASPSRHG---RRLPNGYYP--HGLARPGPGSRKKGHLHE 970
QY 144 SSS 146
Db 971 PYS 973

RESULT 12
Q9NS88 PRELIMINARY; PRT; 2506 AA.
AC Q9NS88:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ALPHA1A-VOLTAGE-DEPENDENT CALCIUM CHANNEL.
GN CACNA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CREBELLUM;
RX MEDLINE=20219126; PubMed=10733886;
RA Toru S., Murakoshi T., Ishikawa K., Saegusa H., Fujigasaki H.,
RA Uchiwara T., Nagayama S., Osanai M., Mizusawa H., Tanabe T.;
RT "Spinocerebellar ataxia type 6 mutation alters P-type calcium channel
RT function."
J. Biol. Chem. 275:10893-10898(2000).
DR EMBL; AB035727; BAA94766.2; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR000637; -.
DR InterPro; IPR001682; -.
DR InterPro; IPR002077; -.
DR InterPro; IPR002111; -.
DR Pfam; PF00520; Ion_trans; 4.
DR PRINTS; PR00167; CACHANNEL.
DR SMART; SM00384; AT_hook; 1.
SQ SEQUENCE 2506 AA; 282580 MW; D64A6C75284A1B53 CRC64;

Query Match 10.68; Score 95.5; DB 4; Length 2506;
Best Local Similarity 25.1%; Pred. No. 2.1;
Matches 46; Conservative 18; Mismatches 50; Indels 69; Gaps 10;

QY 15 SSSAERGLGPS--AGDPSGSGKHHROAP-----GLLWDAS- 49
Db 2335 TSGPRPRPGPTAEPLAGDRPTGHSRSPMERVRPGPARSPRACRHGGARWPASG 2394
QY 50 -HOOEQPTSSHHHGAGCAVEIRSRHSSYPAGTDEDE-----GMGEE-----PSPFR 94
Db 2395 PHVSEGGPPRRHG-----YRGSYDEADPGSGGEEAMAGAYDAPPVVR 2441
QY 95 -----GRS-----RSAPPNLWAQRYGRELRRMXDEFVDSFKKGLPRPKSAGTATQMRQ 143
Db 2442 HASSGATGRSPRTPRASGPACASPSRHG---RRLPNGYYP--HGLARPGPGSRKKGHLHE 2496
QY 144 SSS 146
Db 2497 PYS 2499

RESULT 13
Q9KNK4 PRELIMINARY; PRT; 923 AA.
AC Q9KNK4:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
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```
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE L5204.2.
DE L5204.2.
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock M.,
RA Cawthra J., Marsolini F., Sunkin S., Stuart K.D.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005941; AAF34290.1; -.
DR InterPro; IPR000533; -.
DR PRINTS; PR00194; TROPOMYOSIN.
SQ SEQUENCE 923 AA; 103964 MW; C229C15F6448F7C7 CRC64;
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Query Match 10.5%; Score 94.5; DB 5; Length 923;
Best Local Similarity 26.4%; Pred. No. 0.93;
Matches 33; Conservative 20; Mismatches 45; Indels 27; Gaps 7;
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```
QY 10 SEQEDSSAERGLGPSAGDPSGSGKHHROAPGLLWDASHQQEQPTSSHHHGAGAVEI 69
Db 802 AEQRTNTDDR-----SPSAGGPASADVEHSA-----SQPQPHS---HAGGSAI-V 845
QY 70 RSRHSSYPAGTDEDEGMGEPSPEGR--SRSAPENLWAQRYGRELRRMXDEFVDSFKK 127
Db 846 SNSHNGVQAAA---SGTGRMSAANSRGRVNGSVPP-----RNGRRRAPLAAILDTLTA 896
QY 128 GLRPL 132
Db 897 GPPQP 901
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```
RESULT 14
Q25734 PRELIMINARY; PRT; 1729 AA.
AC Q25734:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE PFEMP1 VARIANT 2 OF STRAIN MC (FRAGMENT).
GN MCVAR-2 PFEMP1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALAYAN CAMP (MC132 K+C+R+);
RX MEDLINE=95330812; PubMed=7541722;
RA Baruch D.I., Pasloske B.L., Singh H.B., Bi X., Ma X.C., Feldman M.,
RA Taraschi T.F., Howard R.J.;
RT "Cloning the P. falciparum gene encoding PFEMP1, a malarial variant
RT antigen and adherence receptor on the surface of parasitized human
RT erythrocytes."
Cell 82:77-87(1995).
RL EMBL; U27339; AAA89134.1; -.
DR NONTER 1729 1729
SQ SEQUENCE 1729 AA; 195156 MW; 7BFEC2131FFBAll CRC64;
```

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Query Match 10.5%; Score 94.5; DB 5; Length 1729;
Best Local Similarity 21.6%; Pred. No. 1.8;
Matches 42; Conservative 23; Mismatches 66; Indels 63; Gaps 8;
```

```
QY 9 PSEQEDSSAERGLGPS--AGDPSGSGKHHROAPGLL-----WDASHHQOEOPTSSSHH 61
Db 926 PSNGESSPEKLPGQPTPETTKETPESSILLHAFVSPPRLRFLPW---HKFAEQWKAOHG 982
QY 62 GGAGAVEIRSRHSSYPAGTDEDEGMGEPSPEGRSRSAPPNLWAQRY----- 110
Db 983 AGATGLQL-----PGVTVD-----SDPDQTLKRGNIPLNDFLQMFYTLGDYRDICI 1031
```

```

Qy 111 -----GRELRMXDEFVDSFKKGLPRKSAGTATQMRQSSWTRVF--- 151
Db 1032 GGDRIIVGDTIVSITGESTKKKIKIEGLFK-----KQVTSFSPRDTSSRTPVHPQT 1086
Qy 152 -----QSWWDRN 158
Db 1087 SVEKTPQQTWWEAN 1100

```

RESULT	15	
QH09B		
ID	QH09B9	PRELIMINARY; PRT; 549 AA.
AC	QH09B9	
DT	01-MAR-2001	(TrEMBLrel. 16, Created)
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)
DT	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)
DE	HYPOTHETICAL 62.2 KDA PROTEIN.	
GN	DKFZF434P2235.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoideae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RP	TISSUE=TESTIS;	
RA	Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;	
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AL136860; CAB66794.1;	
KQ	Hypothetical protein.	
SW	SEQUENCE	549 AA; 06F7BD388F2169A8 CRC64;

Search completed: October 9, 2001, 16:03:21
Job time: 306 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:57:35 ; Search time 33.29 seconds
(without alignments)
305.943 Million cell updates/sec

Title: 09-580523-1a
Perfect score: 902
Sequence: 1 MFQIPFEPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
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4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	99.9	168	19	AAW55779 Human Bcl-xL/Bcl-2
2	901	99.9	168	21	AAB13512 Human cell prolif
3	901	99.9	168	22	AAB70368 Human BAD mutant a
4	901	99.9	168	22	AAB48287 Human BAD protein.
5	747	82.8	166	18	AAB32476 BBC6 protein for r
6	645	71.5	162	22	AAB70370 Shorter murine BAD
7	645	71.5	204	17	AAR95168 bcl-x(L)/bcl-2 ass
8	645	71.5	204	19	AAW61315 Murine BCL-XL/BCL-
9	645	71.5	204	19	AAW58832 Murine BAD protein
10	645	71.5	204	22	AAB70369 Longer murine BAD
11	642	71.2	204	19	AAW61317 Mutant BCL-XL/BCL-

12	639	70.8	204	19	AAW61316	Mutant BCL-XL/BCL-
13	639	70.8	204	19	AAW61318	Mutant BCL-XL/BCL-
14	310	34.4	59	19	AAW61319	Mutant BCL-XL/BCL-
15	310	34.4	59	19	AAW61320	Mutant BCL-XL/BCL-
16	307	34.0	59	19	AAW61321	Mutant BCL-XL/BCL-
17	304	33.7	59	19	AAW61322	Mutant BCL-XL/BCL-
18	159	17.6	56	21	AAW02251	Human secreted pro
19	129	14.3	26	21	AAW96321	Mammalian Bad Bcl-
20	129	14.3	26	22	AAB70371	BAD BH3 consensus
21	116.5	12.9	27	21	AAB37003	Bcl2 polypeptide B
22	112	12.4	23	17	AAR95166	bcl-x(L)/bcl-2 ass
23	110	12.2	26	21	AAB37001	Bcl2 polypeptide B
24	110	12.2	26	21	AAB37002	Bcl2 polypeptide B
25	110	12.2	27	21	AAB37056	Bcl2 polypeptide B
26	110	12.2	28	21	AAB37055	Bcl2 polypeptide B
27	96	10.6	2510	16	AAR71007	Human neuronal cal
28	96	10.6	2510	21	AAB10579	Human calcium chan
29	95.5	10.6	1182	20	AAB33496	Human SCA6 protein
30	94.5	10.5	395	21	AAW91951	Human cytoskeleton
31	94.5	10.5	1726	17	AAW00385	Truncated Plasmodi
32	94	10.4	1931	13	AAR27649	Human calcium chan
33	93.5	10.4	549	21	AAW84901	A human proliferat
34	93.5	10.4	1447	20	AAW81029	Murine pcip protei
35	90	10.0	434	17	AAB96420	Peptide fragment o
36	90	10.0	434	21	AAB12821	Human N-type calci
37	90	10.0	2237	16	AAR71006	Human neuronal cal
38	90	10.0	2237	19	AAW63142	Human calcium chan
39	90	10.0	2237	21	AAB10573	Human calcium chan
40	90	10.0	2337	19	AAW37878	Human calcium chan
41	90	10.0	2339	14	AAR33549	Sequence of the al
42	90	10.0	2339	16	AAR71005	Human neuronal cal
43	90	10.0	2339	19	AAW63141	Human calcium chan
44	90	10.0	2339	21	AAB10572	Human calcium chan
45	90	10.0	2343	20	AAW31809	N-type calcium cha

ALIGNMENTS

RESULT 1	
AAW55779	AAW55779 standard; Protein; 168 AA.
ID	AAW55779 standard; Protein; 168 AA.
XX	
AC	AAW55779;
XX	
XX	
DT	17-JUL-1998 (first entry)
XX	
DE	Human Bcl-xL/Bcl-2 associated death promoting polypeptide.
XX	
KW	Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;
KW	programmed cell death; apoptosis.
XX	
OS	Homo sapiens.
XX	
PN	WO9812328-A2.
XX	
PD	26-MAR-1998.
XX	
PF	18-SEP-1997; 97WO-US16991.
XX	
PR	20-SEP-1996; 96US-0717123.
XX	
PA	(IDUN-) IDUN PHARM INC.
XX	
PI	Horne WA, Oltersdorf T;
XX	
DR	BBC6 protein for r
XX	
XX	WPI; 1998-217267/19.
XX	N-PSDB; AAV25877.
PT	Bad gene mediating apoptosis - used to develop products for treating
XX	e.g. neurodegenerative disease, cancers or autoimmune disease
PS	Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL
 CC results in the induction of programmed cell death, i.e. apoptosis.
 CC Bad can be used in screening assays for compounds to treat or
 CC prevent diseases characterised by apoptotic cell death, such as
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
 CC aplastic anaemia and ischaemic injury including myocardial
 CC infarction, stroke and reperfusion injury. Assays can also be
 CC used to obtain apoptosis enhancing compounds to treat or prevent
 CC diseases characterised by the loss of apoptotic cell death, such as
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated
 CC glomerulonephritis and viral infections, e.g. herpesvirus,
 CC poxvirus or adenovirus infection. Bad can also be used for
 CC detection and diagnosis.
 XX
 SQ Sequence 168 AA;

Query Match 99.9%; Score 901; DB 19; Length 168;
 Best Local Similarity 99.4%; Pred. No. 3.4e-87;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPCLLWDASHQOQPTSSSH 60
 DB 1 mfiqifefsepqedsssaeriglpagdgpgsgkhrrqapglldashhqqeqptcssh 60
 QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMXDE 120
 DB 61 hgagaveirsrhssypagteddegmggeppsfgrgrsappnlwaaqrygrellrmsde 120
 QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
 DB 121 fvdskkglprpksgagtatqmrqssswtrvfqswmdrnlgrgssapsq 168

RESULT 2

AAB13512
 ID AAB13512 standard; protein; 168 AA.
 AC AAB13512;
 XX
 XX
 DT 02-NOV-2000 (first entry)
 XX
 XX Human cell proliferation protein APOP-1.
 DE
 XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.
 KW
 XX Homo sapiens.
 OS
 XX US6080847-A.
 PN
 XX 27-JUN-2000.
 PD
 XX
 XX 04-DEC-1997; 97US-0985335.
 PF
 XX 04-DEC-1997; 97US-0985335.
 PR
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;
 PI
 XX WPI; 2000-451230/39.
 DR N-PSDB; AAA63332.
 DR
 XX Novel polynucleotide and polypeptide sequences of proteins associated
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.
 PT Cancer, acquired immunodeficiency syndrome, and Parkinson's disease -
 XX

Example 8; Fig 1; 58pp; English.

PS The present sequence is the human APOP-1 protein. This protein, which
 XX shares structural and chemical homology with Bcl-2, is involved in cell
 CC proliferation. Its coding sequence was isolated by screening a synovial
 CC tissue cDNA library using a computer search for amino acid sequence
 CC alignments. The gene and protein can be used in the treatment of various
 CC cancers, disorders with associated inflammation such as Addison's
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
 CC of cancer, haemodialysis and extracorporeal circulation, infections,
 CC trauma, disorders with associated apoptosis including AIDS and other
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
 CC such as myocardial infarction, and wasting diseases including cachexia.
 XX
 SQ Sequence 168 AA;

Query Match 99.9%; Score 901; DB 21; Length 168;

Best Local Similarity 99.4%; Pred. No. 3.4e-87;

Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSSGKHHRQAPCLLWDASHQOQPTSSSH 60

DB 1 mfiqifefsepqedsssaeriglpagdgpgsgkhrrqapglldashhqqeqptsssh 60

QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMXDE 120

DB 61 hgagaveirsrhssypagteddegmggeppsfgrgrsappnlwaaqrygrellrmsde 120

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

DB 121 fvdskkglprpksgagtatqmrqssswtrvfqswmdrnlgrgssapsq 168

RESULT 3

AAB70368
 ID AAB70368 standard; protein; 168 AA.

AC AAB70368;

DT 02-MAY-2001 (first entry)

DE Human BAD mutant amino acid sequence SEQ ID NO:1.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.

OS Homo sapiens.

OS Synthetic.

XX WO200110888-A1.

XX 15-FEB-2001.

XX 30-MAY-2000; 2000WO-US11864.

XX 28-MAY-1999; 99US-0136783.

XX (APOP-) APOPTOSIS TECHNOLOGY INC.

XX Zhou X;

XX

DR WPI; 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Claim 1; Page 147; 157pp; English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC neurotropic, antiischaemic, vulnerary, cytostatic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed human BAD mutant amino acid sequence from the present invention.
 XX
 SQ Sequence 168 AA;

Query Match 99.9%; Score 901; DB 22; Length 168;
 Best Local Similarity 99.4%; Pred. No. 3.4e-87;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60
 Db 1 mfiqipefepseqedsssaerglgpspagdgpssgkhhrrqapglldashhqqeqtsssh 60
 Qy 61 HGGAGAVIRSRHSSYPAGTDEDCMGEEPPFRCGRSRAPPNLWAAQRYGRELRRMXDE 120
 Db 61 hggagaveirsrhssypagtdedgmgeepfgrgrsrappnlwaaqrygreilrrmsde 120
 Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRLNLRGSSAPSQ 168
 Db 121 fvdskfkgllprpksgatqmrqsswtrvfgswmdrnlgrgssapsq 168

RESULT 4
 AAB48287
 ID AAB48287 standard; protein; 168 AA.
 XX
 AC AAB48287;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human Bad protein.
 XX
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200075184-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 05-JUN-2000; 2000WO-US15449.
 XX
 PR 04-JUN-1999; 99US-0137494.
 XX
 PA (UYVA) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;
 XX WPI; 2001-061703/07.
 DR N-PSDB; AAC84599.
 XX
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 XX
 PS Claim 5; Page 102-103; 162pp; English.
 XX
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/ CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 XX
 SQ Sequence 168 AA;
 Query Match 99.9%; Score 901; DB 22; Length 168;
 Best Local Similarity 99.4%; Pred. No. 3.4e-87;
 Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MFQIPEFPEPSEQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60
 Db 1 mfiqipefepseqedsssaerglgpspagdgpssgkhhrrqapglldashhqqeqtsssh 60
 Qy 61 HGGAGAVIRSRHSSYPAGTDEDCMGEEPPFRCGRSRAPPNLWAAQRYGRELRRMXDE 120
 Db 61 hggagaveirsrhssypagtdedgmgeepfgrgrsrappnlwaaqrygreilrrmsde 120
 Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDRLNLRGSSAPSQ 168
 Db 121 fvdskfkgllprpksgatqmrqsswtrvfgswmdrnlgrgssapsq 168
 RESULT 5
 AAW32476
 ID AAW32476 standard; protein; 166 AA.
 XX
 AC AAW32476;
 XX
 DT 15-JAN-1998 (first entry)
 XX
 DE BBC6 protein for regulating cell death.
 XX
 KW BBC6 gene; cell death; cell cycle; Bcl2; human.
 XX
 OS Homo sapiens.
 XX
 PN US5663316-A.
 XX
 PD 02-SEP-1997.
 XX
 PF 18-JUN-1996; 96US-0665617.
 XX
 PR 18-JUN-1996; 96US-0665617.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Xudong Y;
 XX
 DR WPI; 1997-447980/41.
 DR N-PSDB; AAT91561.
 XX
 PT Isolated BBC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2

XX PS Claim 1; Column 11-12; 7pp; English.

CC The present sequence represents a protein of 166 amino acids. The

CC sequence is disclosed as being a protein called Bcl-2. The DNA may be used for the

CC cell death through interaction with Bcl-2. The DNA may be used for the

CC production of the recombinant protein, which can be used in unspecified

CC therapeutic or diagnostic procedures, as a molecular weight marker, and

CC to raise antibodies that can be used in unspecified diagnostic or

CC therapeutic applications and to reduce or eliminate the biological

CC activity of the Bcl-2 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 82.8%; Score 747; DB 18; Length 166;

Best Local Similarity 83.4%; Pred. No. 5.4e-71;

Matches 146; Conservative 3; Mismatches 10; Indels 16; Gaps 3;

QY 1 MFOIPEFPESEQDSSAERGLGPGSPAGDPSGSGKHRRQAPG-----LLWDASHQOE 53

DB 1 mfiqipefpeqedssaaerg-wrspagtp-----qapasiiarpqvlwdashqge 51

QY 54 QPTSSHHGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPNLWAAQRYGRE 113

DB 52 qptssshhgagaveirsrhssypagtdedgmgeepsfrgrararppnlwaaqrygre 111

QY 114 LRRMDEFDVDFSKKGLPRPKSAGTATQMRQSSWTRVFSWMDRNLGRGSSAPSQ 168

DB 112 lrmsdefvdfskglprpksgatqmrqsswtrvfgswdrnlgrgtaapsq 166

RESULT 6

AAB70370

ID AAB70370 standard; protein; 162 AA.

XX AC AAB70370;

XX DT 02-MAY-2001 (first entry)

XX DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

XX KW immunostimulant; neuroprotective; nontropic; antischismatic; vulnary;

XX KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

XX KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

XX KW immunodeficiency disease; neurodegenerative disease; viral infection;

XX KW ischaemic cell death; reperfusion cell death; arthritis; infertility;

XX KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.

XX OS Synthetic.

XX PN WO200110888-A1.

XX PD 15-FEB-2001.

XX PF 30-MAY-2000; 2000WO-US11864.

XX PR 28-MAY-1999; 99US-0136783.

XX PA (APOP-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX DR WPI; 2001-138734/14.

XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,

XX PT useful for screening for candidate compounds which induce or inhibit

XX PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or

XX PT Ser113 -

XX PS Claim 7; Page 148-149; 157pp; English.

XX CC The present invention describes an isolated or synthetic polypeptide

CC (1) comprising a less than full length amino acid sequence of a mutant

CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

CC fragment, which contains amino acid substitutions at Ser118 of a human

CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,

CC nontropic, antischismatic, vulnary, cytostatic, antiviral,

CC antiarthritic, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC identified and (mutant) BAD polypeptides are useful in treating

CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

CC death, reperfusion cell death, wound healing, cancer, viral infections,

CC lymphoproliferative conditions, arthritis, infertility, inflammation and

CC autoimmune diseases. The present sequence represents a specifically

CC claimed shorter murine BAD mutant amino acid sequence from the present

CC invention.

XX SQ Sequence 162 AA;

Query Match 71.5%; Score 645; DB 22; Length 162;

Best Local Similarity 75.0%; Pred. No. 2.9e-60;

Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

QY 1 MFOIPEFPESEQDSSAERGLGPGSPAGDPSGSGKHRRQAPGLLWDASHQOEPTSSSH 60

DB 1 mfiqipefpeqedssaatdrglpsltedqp---gpy--lapglgslnhqggraatsnsh 55

QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPNLWAAQRYGRELRMXDE 120

DB 56 hggagaveirsrhssypagteedgmeeelsprgrsrsappnlwaaqrygrelrmsde 115

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFSWMDRNLGRGSSAPSQ 168

DB 116 fegsf-kglprpksgatqmrqsgatrligswdrnlgrgsgtspq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AC AAR95168;

XX DT 06-JAN-1997 (first entry)

XX DE bcl-x(L)/bcl-2 associated death promoter protein.

XX KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

XX KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;

XX KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

XX KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX OS Mus musculus.

XX FH Location/Qualifiers

FT Key 147..149

FT Region /note="BH1 conserved amino acids"

FT Region 191..192

FT Domain /note="BH2 conserved amino acids"

FT FT 38..61

FT FT /note="PEST sequence"

FT FT 111..130

FT FT /note="PEST sequence"

XX PN WO9613614-A1.

XX PD 09-MAY-1996.

XX PF 31-OCT-1995; 95WO-US14246.

```
XX PR 31-OCT-1994; 94US-0333565.
XX PA (UNITW ) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX XX
DR WPI; 1996-251465/25.
DR N-PSDB; AAT29479.
XX
XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
PT useful to treat neoplasia and apoptosis and to identify agents
PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
XX
XX Claim 3; Fig 1; 130pp; English.
XX
XX This sequence represents the murine bcl-x(L)/bcl-2 associated death
CC promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
CC to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad
CC has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
CC death inhibitory activity of bcl-x(L), but is much less effective at
CC countering the death inhibitory activity of bcl-2. Bad expression can
CC accelerate apoptotic cell death induced by cytokine deprivation in an
CC IL-3 dependent cell line expressing bcl-x(L), and its also counters the
CC death repressor activity of bcl-x(L). Bad competes with Bax for binding
CC to bcl-x(L). Bad may be used to identify agents which inhibit its
CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
CC used to treat neurodegenerative diseases, immunodeficiency diseases,
XX e.g. AIDS, senescence or ischaemia.
XX
SQ Sequence 204 AA;

Query Match 71.5%; Score 645; DB 17; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.8e-60;
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

Qy 1 MFQIPEFPSPQEDSSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
Db 43 mfiqefepsegedasatdrglpsltedqp---gpy--lapglgslnhqgggraatsnsh 97

Qy 61 HGGAGAVEIRSHSSYPAGTDEDEGMGEPSPFGRGRSAPPNLWAAQRYGRELRMXDE 120
Db 98 hggagameirshssypagteedegmeelspfgrgrsappnlwaaqrygreilrmsde 157

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
Db 158 fegsf-kglprpkasagtatqmrqagwtriiqswdrnlkggstpsq 204

RESULT 8
AAW61315
ID AAW61315 standard; Protein; 204 AA.
XX
XX AAW61315;
XX
XX 07-OCT-1998 (first entry)
XX
XX Murine BCL-XL/BCL-2 associated cell death regulator.
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX Mus sp.
XX
XX WO9817682-A1.
XX
XX 30-APR-1998.
XX
XX 17-OCT-1997; 97WO-US19175.
XX
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PR 18-OCT-1996; 96US-0733505.
XX (UNITW ) UNIV WASHINGTON.
XX PI Korsmeyer SJ;
XX XX
DR WPI; 1998-261422/23.
DR N-PSDB; AAV27833.
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 1; Fig 10; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence is the murine BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX
SQ Sequence 204 AA;

Query Match 71.5%; Score 645; DB 19; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.8e-60;
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;

Qy 1 MFQIPEFPSPQEDSSSAERGLGSPAGDGPSSGSKHHRQAPGLLWDASHOQPTSSSH 60
Db 43 mfiqefepsegedasatdrglpsltedqp---gpy--lapglgslnhqgggraatsnsh 97

Qy 61 HGGAGAVEIRSHSSYPAGTDEDEGMGEPSPFGRGRSAPPNLWAAQRYGRELRMXDE 120
Db 98 hggagameirshssypagteedegmeelspfgrgrsappnlwaaqrygreilrmsde 157

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
Db 158 fegsf-kglprpkasagtatqmrqagwtriiqswdrnlkggstpsq 204

RESULT 9
AAW58832
ID AAW58832 standard; protein; 204 AA.
XX
XX AAW58832;
XX
XX 23-JUL-1998 (first entry)
XX
XX Murine BAD protein.
XX
XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
XX serine phosphorylation; post-translational modification; apoptosis;
XX signal transduction regulator; phosphoserine phosphatase; senescence;
XX immunodeficiency disease; neurodegenerative disease; infertility;
```

KW cancer, viral infection; lymphoproliferative condition; arthritis;
KW inflammation; autoimmune diseases.
OS Mus sp.
XX WO9809643-A1.
PN 12-MAR-1998.
XX 09-SEP-1997; 97WO-US15871.
PD 09-SEP-1996; 96US-0707868.
XX (UNIV) UNIV WASHINGTON.
PR Kormsmeier SJ;
XX WPI; 1998-207049/18.
XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
XX polypeptide - useful for modulation of apoptosis associated with,
XX e.g. cancer and immunodeficiency diseases
XX Claim 3; Fig 8; 61pp; English.
XX This sequence represents a novel serine-phosphorylated protein, BAD
XX (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
XX phosphorylated in a post-translational modification and allows binding
XX to the 14-3-3 protein which is a signal transduction regulator.
XX Modulators of phosphorylated BAD, which act through inhibition/activation
XX of a phosphoserine phosphatase, are useful for preventing/treating
XX increased/decreased apoptosis in a cell. The increased apoptosis may
XX result from immunodeficiency diseases, senescence, neurodegenerative
XX disease, ischaemic cell death, reperfusion cell death, infertility and
XX wound-healing. Decreased apoptosis may result from cancer, viral
XX infection, lymphoproliferative conditions, arthritis, infertility,
XX inflammation and autoimmune diseases. Measuring the amount of
XX phosphorylated compared to unphosphorylated BAD polypeptide and/or total
XX BAD in a cell is useful for determining the apoptotic state of a cell.
XX Sequence 204 AA;
Query Match 71.5%; Score 645; DB 19; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.8e-60;
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHRRQAPGLLWDASHQQPQTSSSH 60
DB 43 mfiqipefepseqedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSFPRGRSRAPPNLMWAQRYGRELRRMXDE 120
DB 98 hggagamestrsrhssypagteedegmeelsprfgrsrappnlwaaqrygrellrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDNLGRGSSAPSQ 168
DB 158 fegsf-kglprksagtatqmrqsagwtrliqswdnlgrgsgstpsq 204
RESULT 10
ID AAB70369
XX AAB70369 standard; protein; 204 AA.
XX AAB70369;
XX 02-MAY-2001 (first entry)
XX Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
KW immunostimulant; neuroprotective; nontropic; antischismatic; vulnary;
KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
KW immunodeficiency disease; neurodegenerative disease; viral infection;
KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
XX lymphoproliferative condition; inflammation; autoimmune disease.
XX Mus musculus.
OS Synthetic.
XX WO200110888-A1.
PN 15-FEB-2001.
XX 30-MAY-2000; 2000WO-US11864.
XX 28-MAY-1999; 99US-0136783.
XX (APOP-) APOPTOSIS TECHNOLOGY INC.
XX Zhou X;
XX WPI; 2001-138734/14.
XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
XX useful for screening for candidate compounds which induce or inhibit
XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
XX Ser113 -
XX Claim 4; Page 148; 157pp; English.
XX The present invention describes an isolated or synthetic polypeptide
XX (I) comprising a less than full length amino acid sequence of a mutant
XX Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
XX fragment, which contains amino acid substitutions at Ser118 of a human
XX BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
XX BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
XX nontropic, antischismatic, vulnary, cytostatic, antiviral,
XX antiarthritic, antiinflammatory and immunosuppressive activities, and
XX can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
XX polynucleotides can be used for screening candidate compounds and drugs
XX for activity that promote cell survival or apoptosis. Other uses include
XX inducing or inhibiting apoptosis in a cell. Candidate compounds
XX identified and (mutant) BAD polypeptides are useful in treating
XX immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
XX death, reperfusion cell death, wound healing, cancer, viral infections,
XX lymphoproliferative conditions, arthritis, infertility, inflammation and
XX autoimmune diseases. The present sequence represents a specifically
XX claimed longer murine BAD mutant amino acid sequence from the present
XX invention.
XX Sequence 204 AA;
Query Match 71.5%; Score 645; DB 22; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.8e-60;
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHRRQAPGLLWDASHQQPQTSSSH 60
DB 43 mfiqipefepseqedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMEEPSFPRGRSRAPPNLMWAQRYGRELRRMXDE 120
DB 98 hggagamestrsrhssypagteedegmeelsprfgrsrappnlwaaqrygrellrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDNLGRGSSAPSQ 168
DB 158 fegsf-kglprksagtatqmrqsagwtrliqswdnlgrgsgstpsq 204
RESULT 11
AAW61317
XX AAW61317 standard; Protein; 204 AA.
XX

Db 43 mfiqlpefepsegedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGCAGAVEIRSRHSYPAGTDEDEGMEERPPRGRSRSAAPPNLWAAQRYGRELRRMXDE 120
Db 98 hggagamestrhsaypagteedegmeelsprgrsraappnlwaaqrygrelrrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 158 fegsf-kglprksagtatqmrqsagwttriigswdwnlrgkgstpsq 204
RESULT 13
AAW61318
ID AAW61318 standard; Protein; 204 AA.
AC AAW61318;
XX
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
DE
DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX Mus sp.
OS Synthetic.
XX
XX WO9817682-Al.
PN
XX
XX 30-APR-1998.
PD
XX
XX 17-OCT-1997; 97WO-US19175.
PF
XX
XX 18-OCT-1996; 96US-0733505.
PR
XX
XX (UNIW) UNIV WASHINGTON.
PA
XX
XX Korsmeyer SJ;
PI
XX
XX WPI; 1998-261422/23.
DR
XX N-PSDB; AAV27836.
DR
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 7; Page 60-61; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX

SQ Sequence 204 AA;
Query Match 70.8%; Score 639; DB 19; Length 204;
Best Local Similarity 73.8%; Pred. No. 1.6e-59;
Matches 124; Conservative 14; Mismatches 24; Indels 6; Gaps 3;
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLMDASHQEQDPTSSSH 60
Db 43 mfiqlpefepsegedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGCAGAVEIRSRHSYPAGTDEDEGMEERPPRGRSRSAAPPNLWAAQRYGRELRRMXDE 120
Db 98 hggagamestrhsaypagteedegmeelsprgrsraappnlwaaqrygrelrrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 158 fegsf-kglprksagtatqmrqsagwttriigswdwnlrgkgstpsq 204
RESULT 14
AAW61319
ID AAW61319 standard; Protein; 59 AA.
XX
XX AAW61319;
XX
XX 07-OCT-1998 (first entry)
XX
XX Mutant BCL-XL/BCL-2 associated cell death regulator #4.
DE
XX
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX Mus sp.
OS Synthetic.
XX
XX WO9817682-Al.
PN
XX
XX 30-APR-1998.
PD
XX
XX 17-OCT-1997; 97WO-US19175.
PF
XX
XX 18-OCT-1996; 96US-0733505.
PR
XX
XX (UNIW) UNIV WASHINGTON.
PA
XX
XX Korsmeyer SJ;
PI
XX
XX WPI; 1998-261422/23.
DR
XX N-PSDB; AAV27837.
DR
XX
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
XX Claim 8; Page 73; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is

QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRELRRMXDE 120
|||||
Db 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 2
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1

Query Match 99.9%; Score 901; DB 3; Length 168;
Best Local Similarity 99.4%; Pred. No. 3.7e-86;
Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQOQPTSSSH 60
|||||
Db 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQOQPTSSSH 60
QY 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRELRRMXDE 120
|||||
Db 61 HGCAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||

Db 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 3
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-617-2

Query Match 82.8%; Score 747; DB 1; Length 166;
Best Local Similarity 83.4%; Pred. No. 3.3e-70;
Matches 146; Conservative 3; Mismatches 10; Indels 16; Gaps 3;
QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPG-----LLWDASHQOE 53
|||||
Db 1 MFOIPEFEPSEQEDSSAERG-WRSPAGTGP-----QAPASIIARQVLDASHQOE 51
QY 54 OPTSSSHHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLMWAAQRYGRE 113
|||||
Db 52 OPTSSSHHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGARARPPNLMWAAQRYGRE 111
QY 114 LRMDXEFVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 112 LRMDXEFVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWWDRNLGRGTAAPSQ 166

RESULT 4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION

RESULT 14
US-08-733-505A-57

```
; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-57

Query Match 34.0%; Score 307; DB 2; Length 59;
Best Local Similarity 96.6%; Pred. No. 3.5e-25;
Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 63 GAGAVEIRSHSSYPAGTDEDEGMGEPPSPRGRSAPPNLWAAQRYGRELRRMXDEF 121
Db 1 GAGAVEIRSHSSYPAGTDEDEGMGEPPSPRGRSAPPNLWAAQRYGRELRRMSDEF 59

RESULT 15
US-08-733-505A-58
; Sequence 58, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:

; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
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; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-58

Query Match 33.7%; Score 304; DB 2; Length 59;
Best Local Similarity 94.9%; Pred. No. 7.2e-25;
Matches 56; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 63 GAGAVEIRSHSSYPAGTDEDEGMGEPPSPRGRSAPPNLWAAQRYGRELRRMXDEF 121
Db 1 GAGAVEIRSHSAYPAGTDEDEGMGEPPSPRGRSAPPNLWAAQRYGRELRRMSDEF 59

Search completed: October 9, 2001, 15:58:34
Job time: 59 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:09 ; Search time 24.69 seconds
(without alignments)
518.320 Million cell updates/sec

Title: 09-580523-lb
Perfect score: 905
Sequence: 1 MFQIPEFSPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	646	71.4	204	2	A55671	bad protein - mous
2	94.5	10.4	1729	2	T18396	erythrocyte membra
3	93	10.3	1300	2	T03166	probable immediate
4	92	10.2	834	2	T42702	hypothetical prote
5	90.5	10.0	393	2	JC5614	RNB6 protein - rat
6	90	9.9	2237	2	T45115	N-type calcium cha
7	90	9.9	2248	2	A35938	profilaggrin - hum
8	90	9.9	2339	2	A42566	omega-conotoxin-se
9	89.5	9.9	336	2	T30757	hypothetical prote
10	88.5	9.8	449	1	A41520	chromogranin A pre
11	88.5	9.8	2715	2	T13049	eyelid - fruit fly
12	88	9.7	222	2	T43500	hypothetical prote
13	87	9.6	645	1	S15901	chromogranin B pre
14	87	9.6	2023	2	T13134	polycomb protein e
15	86.5	9.6	1077	2	A44067	serine-rich protein
16	86.5	9.6	1647	2	S45252	SNF2beta protein -
17	86	9.5	343	2	T05221	hypothetical prote
18	86	9.5	420	2	B38104	LFY floral meriste
19	85.5	9.4	751	2	T02858	hypothetical prote
20	85.5	9.4	1159	2	T38465	probable potassium
21	85	9.4	270	1	WJMS13	homeotic protein H
22	84.5	9.3	134	2	T54810	pHL E1F1 - human
23	84.5	9.3	1323	2	T00037	hypothetical prote
24	84.5	9.3	1392	2	T51947	probable transcrip
25	84.5	9.3	1562	2	T29146	hypothetical prote
26	84	9.3	313	2	A28444	filaggrin precurs
27	84	9.3	380	2	S51797	vasodilator-stimul
28	84	9.3	381	2	S16506	hypothetical prote
29	84	9.3	542	2	A44358	zyxin - chicken

ALIGNMENTS

RESULT 1

A55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes apoptosis
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779
C:Keywords: heterodimer

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.le-45;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

Qy 1 MFQIPEFSPSEQEDSSAERGLGSPAGDGSGCKHHRQAPGLLDASHQEQPTSSSH 60
Db 43 MFQIPEFSPSEQEDSATDRGLGSLTEDQP---GPY--LAPGLGSLNIHQGRATNSH 97
Qy 61 HGGAGAVEIRSHSSYPAGTEDDECGEGEPPFRGSRSPAPNLWAAQRYGRELRRMADE 120
Db 98 HGGAGAMETRSRSHSSYPAGTEDECGEELSFPFRGSRSPAPNLWAAQRYGRELRRMSDE 157
Qy 121 FVDSFKGLPRPKSAGTATQMRQSSWTRVQSWDRNLGRGSSAPSQ 168
Db 158 FEGSP-KGLPRPKSAGTATQMRQSGWTRIIQSWDRNLGRGSGSTPSQ 204

RESULT 2

T18396
erythrocyte membrane protein variant 2 - malaria parasite (Plasmodium falciparum) (fr
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T18396
R:Baruch, D.I.; Pasloske, B.L.; Singh, H.B.; Bi, X.; Ma, X.C.; Feldman, M.; Taraschi,
Cell 82, 77-87, 1995
A:Title: Cloning the P. falciparum gene encoding PfEMP1, a malarial variant antigen a
A:Reference number: T18925; MUID:95330812
A:Accession: T18396
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1729 <BAR>
A:Cross-references: EMBL:U27339; NID:g914920; PID:g914921; PIDN:AAA89134.1
C:Genetics:
A:Gene: EMP1

A:Note: var-2

Query Match 10.4%; Score 94.5; DB 2; Length 1729;
Best Local Similarity 21.6%; Pred. No. 8.3;
Matches 42; Conservative 23; Mismatches 66; Indels 63; Gaps 8;
QY 9 PSQEDSSAERGLGSP--AGDGPSCGKHHRAQAGLL-----WDASHQEQPTSSSH 61
DB 926 PSQEDSSAERGLGSP--AGDGPSCGKHHRAQAGLL-----WDASHQEQPTSSSH 982
QY 62 GGAGVEIKRHSYPAGTDEGMEEPSPPFRGRSRAPPNLWAAQRY----- 110
DB 983 AGATGLQL-----SDPDQQLKRGNIPLDFRQMFYTLGDYRDICI 1031
QY 111 -----GRELRRMADEFVDSFKKGLPRPKSAGTATQMRSSSWTRVF--- 151
DB 1032 GGDRIIVGDTIVITGEGSTKKISKIIEGFLK-----KQTVTSPSPRDTSSRTPVHPQT 1086
QY 152 -----QSWDRN 158
DB 1087 SVEKTPQTWWEAN 1100

RESULT 3
T03166
probable immediate early protein - alcelaphine herpesvirus 1
C:Species: alcelaphine herpesvirus 1
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Nov-1999
C:Accession: T03166
R:Enser, A.; Pfanz, R.; Fleckenstein, B.
J. Virol. 71, 6517-6525, 1997
A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.
A:Reference number: 214840; MUID:97404659
A:Accession: T03166
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1300 <ENS>
A:Cross-references: EMBL:AF005370; NID:g2337967; PIDN:AAC58118.1; PID:g2338034
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology

Query Match 10.3%; Score 93; DB 2; Length 1300;
Best Local Similarity 29.0%; Pred. No. 8;
Matches 31; Conservative 6; Mismatches 56; Indels 14; Gaps 3;
QY 5 PEPESEQEDSSAERGLGP-SPAGDGPSCGKHHRAQAGLLWDASHQEQPTSSSHHG 63
DB 466 PEGEPERPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 521
QY 64 AGAVEIRSRHSYPAGTDEGMEEP-----PSPFGRGRSRAP 101
DB 522 EGPEGLEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEGPEG 568

RESULT 4
T42702
hypothetical protein DKFZp434F117.1 - human (fragment)
N:Alternate names: hypothetical protein DKFZp434B239.1
C:Species: Homo sapiens (man)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C:Accession: T42702; T46502
R:Koehler, K.; Beyer, A.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, November 1999
A:Reference number: 222234
A:Accession: T42702
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-834 <AAA>
A:Cross-references: EMBL:AL133028
A:Experimental source: adult testis; clone DKFZp434F117
R:Poustka, A.; Klein, M.; Meves, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000

A:Reference number: 223029
A:Accession: T46502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 213-834 <AA2>
A:Cross-references: EMBL:AL137336
A:Experimental source: adult testis; clone DKFZp434B239
C:Genetics:
A:Note: DKFZp434F117.1; DKFZp434B239.1

Query Match 10.2%; Score 92; DB 2; Length 834;
Best Local Similarity 27.1%; Pred. No. 6;
Matches 49; Conservative 18; Mismatches 50; Indels 64; Gaps 11;
QY 13 EDSSSAERGLGSP--AGDGPSCGKHHRAQAGLLWDASHQEQPTSSSHHGAGAVEI 69
DB 226 EKKHAEAPAGENPPRGPGDARAGSK-----AKPQESPSSAS--ALAEMASI 272
QY 70 RSR-----HSSYPAGTDEDE-GMGEESP-----FRGRSRAPP-----NLMAAQRY--- 110
DB 273 RSRILKNAESDPRSSERDQLRPGDESTPRGRCDSRGNQRKTPPVNAKFSIMPWQKESDG 332
QY 111 GRELRMADEFVDSFKK-----GLPRPKSAGTATQMRSSSWTRVFQSWMDRNLGR 161
DB 333 GTETSKOSTE-AESIRKRPMLGPSEETAPQPPAGV-----RELK 372
QY 162 G 162
DB 373 G 373

RESULT 5
JC5614
RNB6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Sep-1997 #sequence_revision 17-Oct-1997 #text_change 05-Nov-1999
C:Accession: JC5614
R:Ohta, S.; Mineta, T.; Kimoto, M.; Tabuchi, K.
Biochem. Biophys. Res. Commun. 237, 307-312, 1997
A:Title: Differential display cloning of a novel rat cDNA (RNB6) that shows high expr
A:Reference number: JC5614; MUID:97415794
A:Accession: JC5614
A:Molecule type: mRNA
A:Residues: 1-393 <OHT>
A:Cross-references: GB:U70211; NID:g2058461; PIDN:AAC53322.1; PID:g2058462
A:Experimental source: brain
C:Comment: this protein belongs to Ena/VASP family member, and is involved in the dev
ion.

Query Match 10.0%; Score 90.5; DB 2; Length 393;
Best Local Similarity 28.2%; Pred. No. 3.5;
Matches 40; Conservative 16; Mismatches 45; Indels 41; Gaps 7;
QY 13 EDSSSAERGLGSPAGDGPSCGKHHRAQAGLLWDASHQEQPTSSSHHGAGAVEIRSR 72
DB 237 EDAS-----GGSPSGTSGS-----DANR-----ASSGGGGGLMEEMNK 271
QY 73 -----HSSYPAGTDEDEGMEEP--SPPRG--RSRAPPNLWAAQRYGRELRMAD 119
DB 272 LLAKRKAASQTDKPADRKEDENQEDPTSPSPGSRATSPQPPNSSEAGRPWERSNSVE 331
QY 120 EFVDSFKKGLPRPKSAGTATQ 141
DB 332 KPVSSL---LSRVKPGAGSVNDV 350

RESULT 6
T45115
N-type calcium channel alpha-1 chain, omega-conotoxin-sensitive [imported] - human
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:03:43 ; Search time 15.11 Seconds
(without alignments)
380.868 Million cell updates/sec

Title: 09-580523-lb
Perfect score: 905
Sequence: 1 MFQIPEFPEQEDSSSAER.....RVFQSWDRNLGRSSAPSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	741	81.9	168	1	BAD_HUMAN
2	646	71.4	204	1	BAD_MOUSE
3	97	10.7	2505	1	CCAA_HUMAN
4	91.5	10.1	2300	1	CYAA_NEUCR
5	90	9.9	2339	1	CCAB_HUMAN
6	87.5	9.7	449	1	CNCA_BOVIN
7	87	9.6	646	1	SGI_BOVIN
8	87	9.6	962	1	ARVC_HUMAN
9	86.5	9.6	1077	1	HLES_DROME
10	86.5	9.6	1461	1	IE18_PRTIF
11	86.5	9.6	1647	1	SN24_HUMAN
12	85.5	9.4	510	1	DMPL_BOVIN
13	85.5	9.4	1159	1	HERG_HUMAN
14	85	9.4	270	1	HXA5_MOUSE
15	84.5	9.3	215	1	ST13_MOUSE
16	84	9.3	380	1	VASP_HUMAN
17	84	9.3	542	1	2YX_CHICK
18	83.5	9.2	1453	1	NKCR_MOUSE
19	83	9.2	263	1	PENK_BOVIN
20	83	9.2	270	1	HXA5_HUMAN
21	83	9.2	591	1	PAK4_HUMAN
22	82.5	9.1	558	1	ROL_HUMAN
23	82.5	9.1	1097	1	CCT_DROME
24	82.5	9.1	1191	1	NKCL_MOUSE
25	82	9.1	336	1	FILA_MOUSE
26	82	9.1	424	1	LFY_ARATH
27	82	9.1	1021	1	MANA_RHOMR
28	82	9.1	1081	1	SPS2_CRAPL
29	82	9.1	1089	1	Y553_HUMAN
30	81.5	9.0	407	1	Z174_HUMAN
31	81.5	9.0	841	1	1B63_MCMVS
32	81	9.0	559	1	PAXI_CHICK
33	80.5	8.9	1411	1	TCOF_HUMAN

ALIGNMENTS

RESULT 1

ID	BAD_HUMAN	STANDARD;	PRT;	168 AA.
AC	Q92934;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	BAD PROTEIN (BCL-2 BINDING COMPONENT 6).			
GN	BAD OR BBC6 OR BCL2L8.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
CC	NCBI_TaxID=9606;			
CC	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;			
RA	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE			
CC	BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL			
CC	HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE			
CC	THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2			
CC	(BY SIMILARITY)			
CC	- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH			
CC	BAX, MCL-1, AL, OR BCL-X(S) (BY SIMILARITY).			
CC	- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.			
CC	- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).			
CC	- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).			
CC	- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U66879; AAB36516.1; -.			
DR	MIN; 603167; -.			
KW	Apoptosis.			
FT	DOMAIN 101 121 BH1.			
FT	DOMAIN 146 163 BH2.			
SQ	SEQUENCE 168 AA; 18408 MW; BDF3D99587C222BE CRC64;			

Query Match	81.9%;	Score 741;	DB 1;	Length 168;
Best Local Similarity	84.5%;	Pred. No. 1.4e-49;		
Matches 142;	Conservative 1;	Mismatches 25;	Indels 0;	Gaps 0;
Qy	1	MFQIPEFPEQEDSSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHHQEQPTSSSH 60		
Db	1	MFQIPEFPEQEDSSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHHQEQPTSSSH 60		
Qy	61	HGGAGAVEIRSHSYYPAGTDEDCMGEEPPSPFRGSRSPAPNLWAAQRYGRELRRMADE 120		
Db	61	HGGRWGCGDPESPQLLPRGDGRRRDGGGAQPFGRGSRSPAPNLWAAQRYGRELRRMSDE 120		

QY 121 FVDSFKGLPRKSAGTATQMRSSSWTRVFQSWDRNLGRSSAPSQ 168
 |||||
 Db 121 FVDSFKGLPRKSAGTATQMRSSSWTRVFQSWDRNLGRSSAPSQ 168

RESULT 2

BAD_MOUSE
 ID BAD_MOUSE STANDARD; PRT; 204 AA.
 AC 061337;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
 GN BAD OR BBC6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Thymus;
 RX MEDLINE=95136361; PubMed=7834748;
 RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
 RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
 RT promotes cell death.";
 RL Cell 80:285-291(1995).
 CC -I- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE
 CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL
 CC HETERODIMORIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
 CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
 CC -I- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
 CC BAX, MCL-1, AL, OR BCL-X(S).
 CC -I- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -I- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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 CC or send an email to license@isb-sib.ch).

 CC EMBL; L37296; AAA64465.1; -;
 CC MGD; MGI:1096330; Bad.
 KW Apoptosis. 138 158 BH1.
 FT DOMAIN 182 199 BH2.
 SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 71.4%; Score 646; DB 1; Length 204;
 Best Local Similarity 75.0%; Pred. No. 2.4e-42;
 Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
 QY 1 MFQIPEPESEQEDSSAERGLGSPAGDGPFGSGKHHRQAPGLLMDASHQEQPQSSSH 60
 |||||
 Db 43 MFQIPEPESEQEDASATDRLGFLSTEDQ---GPY--LAPGLLGSNIHQGRATNSH 97
 |||||
 QY 61 HGGAGAVEIRSRHSSYPAGTTEDEMGCEPSPFGRSRSAPPNLWAAQRYGRELRLMADE 120
 |||||
 Db 98 HGGAGAMETRSRHSYPAGTTEDEMGCEPSPFGRSRSAPPNLWAAQRYGRELRLMSDE 157
 |||||
 QY 121 FVDSFKGLPRKSAGTATQMRSSSWTRVFQSWDRNLGRSSAPSQ 168
 |||||
 Db 158 FEGSF-KGLPRKSAGTATQMRSSAGWTRIIQSWDRNLKGGSTPSQ 204
 |||||
 RESULT 3
 ID CCAA_HUMAN STANDARD; PRT; 2505 AA.

AC 000555; Q92690; Q16290; Q99790; Q99791; Q99792; Q99793; Q99793; P78510;
 AC P78511;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT (CALCIUM
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 4) (BRAIN CALCIUM CHANNEL
 DE I) (BI).
 OS CACNALA OR CACNL1A4 OR CACH4 OR CACN3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS BI-1-GGCAG/1A-1 AND BI-1/1A-2).
 RC TISSUE=Neuron;
 RX MEDLINE=99158614; PubMed=10049321;
 RA Hans M., Urrutia A., Deal C., Brust P.F., Stauderman K., Ellis S.B.,
 RA Harpold M.M., Johnson E.C., Williams M.E.;
 RT "Structural elements in domain IV that influence biophysical and
 RT pharmacological properties of human alpha1A-containing
 RT high-voltage-activated calcium channels.";
 RL Biophys. J. 76:1384-1400(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BI-1(V1)), AND VARIANTS FHM.
 RC TISSUE=Cerebellum;
 RX MEDLINE=97053792; PubMed=8898206;
 RA Ophoff R.A., Terwindt G.M., Vergouwe M.N., van Eijk R., Oefner P.J.,
 RA Hoffman S.M.G., Lamerding J.E., Mohrenweiser H.W., Bulman D.E.,
 RA Ferrari M., Haan J., Lindhout D., van Ommen G.-J.B., Hofker M.H.,
 RA Ferrari M.D., Frants R.R.;
 RT "Familial hemiplegic migraine and episodic ataxia type-2 are caused by
 RT mutations in the Ca2+ channel gene CACNL1A4.";
 RL Cell 87:543-552(1996).
 RN [3]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain;
 RX MEDLINE=97141920; PubMed=8988170;
 RA Zhuchenko O., Bailey J., Bonnen P.E., Ashizawa T., Stockton D.W.,
 RA Amos C., Dobyns W.B., Subramony S.H., Zoghbi H.Y., Lee C.C.;
 RT "Autosomal dominant cerebellar ataxia (SCA6) associated with small
 RT polyglutamine expansions in the alpha 1A-voltage-dependent calcium
 RT channel.";
 RL Nat. Genet. 15:62-69(1997).
 RN [4]
 RP SEQUENCE OF 1693-1807 FROM N.A.
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=95123449; PubMed=7823133;
 RA Barry E.L.R., Viglione M.P., Kim Y.I., Froehner S.C.;
 RT "Expression and antibody inhibition of P-type calcium channels in
 RT human small-cell lung carcinoma cells.";
 RL J. Neurosci. 15:274-283(1995).
 RN [5]
 RP SEQUENCE OF 2038-2258 FROM N.A.
 RC TISSUE=Frontal cortex;
 RX MEDLINE=96102310; PubMed=8525433;
 RA Margolis R.L., Bressel T.S., Li S.H., Kidwai A.S., Antonarakis S.E.,
 RA McInnis M.G., Ross C.A.;
 RT "Characterization of cDNA clones containing CCA trinucleotide repeats
 RT derived from human brain.";
 RL Somat. Cell Mol. Genet. 21:279-284(1995).
 CC -I- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1A
 CC GIVES RISE TO P AND/OR Q-TYPE CALCIUM CURRENTS. P/Q-TYPE CALCIUM
 CC CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND
 CC ARE BLOCKED BY THE FUNNEL TOXIN (FTX) AND BY THE OMEGA-AGATOXIN-
 CC IVA (OMEGA-AGA-IVA). THEY ARE HOWEVER INSENSITIVE TO
 CC DIHYDROPYRIDINES (DHP), AND OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-
 CC GVIA).
 CC -I- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT


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RESULT 4
CYAA_NEUCR STANDARD; PRT; 2300 AA.
AC Q01631;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLAL
DE CYCLASE).
GN CR-1 OR NAC.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=92000795; PubMed=16803356;
RA Kore-Eda S., Murayama T., Uno I.;
RT "Isolation and characterization of the adenylate cyclase structural
RT gene of Neurospora crassa."
RL Jpn. J. Genet. 66:317-334(1991).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
CC METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CC CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.
CC -!- SIMILARITY: BELONGS TO ADENYLATE CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 23 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN.
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CC -----
CC EMBL: D00909; BAA0755.1; -
CC InterPro: IPR001611; -
CC InterPro: IPR001932; -
CC Pfam: PF00560; LRR; 13.
CC Pfam: PF00481; PP2C; 1.
CC PROSITE: PR00019; LEUZYCHRP.
CC PROSITE: PS00125; GUANYLATE CYCLASES_2; 1.
KW Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT REPEAT 867 890
FT REPEAT 892 914
FT REPEAT 915 938
FT REPEAT 938 961
FT REPEAT 962 986
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CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-1B-1 (SHOWN HERE) AND
 CC ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE
 CC CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.
 CC -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -!- PH: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND GPK
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC EMBL; M94172; AAA51897.1; -;
 CC EMBL; M94173; AAA51898.1; -;
 CC EMBL; U76666; AAC51138.1; -;
 CC MIM: 601012; -;
 CC InterPro: IPR000636; -;
 CC InterPro: IPR002077; -;
 CC Pfam: PF00520; Ion_trans; 4;
 CC PRINTS: PR00167; CACHANNEL.
 CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Calcium channel; Glycoprotein; Repeat; Multigene family;
 CC Calcium-binding; Phosphorylation; ATP-binding; Alternative splicing.
 FT REPEAT 82 359 I.
 FT REPEAT 468 712 II.
 FT REPEAT 1137 1419 III.
 FT REPEAT 1456 1711 IV.
 FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 114 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 115 132 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 133 152 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 153 163 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 164 183 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 184 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 206 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 207 225 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 226 245 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 246 331 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 332 356 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 357 482 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 483 501 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 502 516 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 517 536 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 537 544 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 545 562 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 563 573 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 574 592 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 593 611 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 612 631 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 632 684 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 685 709 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 710 1151 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1152 1169 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1170 1185 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1186 1205 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1206 1217 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1218 1236 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1237 1246 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1247 1265 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1266 1284 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1285 1304 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1305 1391 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1392 1416 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1417 1471 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1472 1490 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1491 1505 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1506 1525 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1526 1533 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1534 1552 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1553 1563 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1564 1582 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1583 1601 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1602 1621 S5 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1622 1683 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1684 1708 S6 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1709 2339 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 2050 2054 POLY-HIS.
 FT DOMAIN 2118 2122 POLY-SER.
 FT DOMAIN 379 396 BINDING TO THE BETA SUBUNIT (BY
 FT SIMILARITY).
 FT NP_BIND 451 ATP (POTENTIAL).
 FT SITE 314 318 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT SITE 563 563 (BY SIMILARITY).
 FT SITE 663 663 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT SITE 1365 1365 (BY SIMILARITY).
 FT SITE 1655 1655 CALCIUM ION SELECTIVITY AND PERMEABILITY
 FT MOD_RES 1719 1719 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CA_BIND 1737 1748 BY SIMILARITY.
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1563 1563 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 2164 2339 TANSPPHFAQAQSLPAPSPGRSLSEHALLQRPDLS
 FT QPLAPSGRIGSDPILQRLDSEASVHALPDTLTFEEAVT
 FT NSGRSSSTSYSSLTSSQSHPLRRVNPNGYHCTGLSSGGRR
 FT HSYHHPDQDHC -> AGSAVGFPNTPCCRETSPASWPL
 FT ALELALTLWGSSVTVRPLSTPCLTRSLRSLRLWPPTRAAP
 FT PGLPTCPP (IN ISOFORM ALPHA-1B-2).
 SQ SEQUENCE 2339 AA; 262494 MW; 17445C6D1E76B39D CRC64;
 Query Match 9.9%; Score 90; DB 1; Length 2339;
 Best Local Similarity 30.8%; Pred. NO. 22;
 Matches 36; Conservative 16; Mismatches 35; Indels 30; Gaps 9;
 QY 8 EPSEQED-----SSSAERGLGPSA-----GDGSGSGKHHKRAQGLLWDA----- 48
 DB 878 EPGAEEERPRPHSHSKAAGPPEARSGRGPGEGGRHRR--GSPEAAEREPRRH 935
 QY 49 -SHQOEQPTSSHHGGAGAV-EIRSRHSYP-AGTDEDEGMGEPS-PFRGRSRAP 101
 DB 936 RAHRHODFSKEC---AGAKGERRARHRRGGPRAGPREAES-GEEPARRHRRHKAQP 987
 RESULT 6
 CMGA_BOVIN STANDARD; PRT; 449 AA.
 ID CMGA_BOVIN STANDARD; PRT; 449 AA.
 AC P05059; P79392;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CHROMOGHRANIN A PRECURSOR (CGA) (PITUITARY SECRETORY PROTEIN 1) (SP-1)
 DE [CONTAINS: VASOSTATIN-1; CHROMOSTATIN; CHROMACIN; PANCREASTATIN; WE-
 DE 14; CATESTATIN].
 GN CHGA.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
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 RP SEQUENCE FROM N.A.

RX MEDLINE-92140395; PubMed-1779968;
RA Iacangelo A.L., Grimes M., Eiden L.E.;
RT "The bovine chromogranin A gene: structural basis for hormone
RT regulation and generation of biologically active peptides.";
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RX SEQUENCE FROM N.A.
RX MEDLINE-86300648; PubMed-3755681;
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RT a class of acidic secretory proteins common to a variety of
RT peptidergic cells.";
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RX MEDLINE-86311345; PubMed-3018587;
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RA Ahn T.G., Cohn D.V., Gorr S.U., Ornstein D.L., Kashdan M.A.,
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RT (chromogranin A) deduced from the cDNA sequence.";
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RT A.";
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RX SEQUENCE OF 142-161, AND SYNTHESIS OF CHROMOSTATIN.
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RX ERRATUM.
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RN [9]
RN
RX SEQUENCE OF 266-312.
RX MEDLINE-89331945; PubMed-2756155;
RA Nakano I., Funakoshi A., Miyasaka K., Ishida K., Makk G., Angwin P.,
RA Chang D., Tatamoto K.;
RT "Isolation and characterization of bovine pancreastatin.";
RL Regul. Pept. 25:207-213(1989).
RN [10]
RN
RX SEQUENCE OF 191-212 (CHROMACIN).
RX TISSUE-Chromaffin granules;
RX MEDLINE-97067080; PubMed-8910482;
RA Strub J.-M., Goumon Y., Lugardon K., Capon C., Lopez M., Moniatte M.,
RA van Dorsselael A., Aunis D., Metz-Boutigue M.-H.;
RT "Antibacterial activity of glycosylated and phosphorylated
RT chromogranin A-derived peptide 173-194 from bovine adrenal medullary
RT chromaffin granules.";
RL J. Biol. Chem. 271:28533-28540(1996).
RN [11]
RN
RX CHARACTERIZATION OF CATESTATIN.
RX MEDLINE-97439785; PubMed-9294131;
RA Mahata S.K., O'Connor D.T., Mahata M., Yoo S.H., Taupenot L., Wu H.,
RA Gill B.M., Parmer R.J.;
RT "Novel autocrine feedback control of catecholamine release. A discrete
RT chromogranin A fragment is a noncompetitive nicotinic cholinergic
RT antagonist.";
RL J. Clin. Invest. 100:1623-1633(1997).
RN [12]
RN
RX CHARACTERIZATION OF CATESTATIN.
RX MEDLINE-99000113; PubMed-9786174;
RA Kennedy B.P., Mahata S.K., O'Connor D.T., Ziegler M.G.;
RT "Mechanism of cardiovascular actions of the chromogranin A fragment
RT catestatin in vivo.";
RL Peptides 19:1241-1248(1998).
RN [13]
RN
RX 3D-STRUCTURE MODELING OF CATESTATIN.
RX MEDLINE-99025667; PubMed-9809795;
RA Tsigelny I., Mahata S.K., Taupenot L., Preece N.E., Mahata M.,
RA Khan I., Parmer R.J., O'Connor D.T.;
RT "Mechanism of action of chromogranin A on catecholamine release:
RT molecular modeling of the catestatin region reveals a beta-
RT strand/loop/beta-strand structure secured by hydrophobic interactions
RT and predictive of activity.";
RL Regul. Pept. 77:43-53(1998).
RN [14]
RN
RX CHARACTERIZATION OF VASOSTATIN-1.
RX MEDLINE-20219105; PubMed-10753865;
RA Lugardon K., Raffner R., Goumon Y., Corti A., Delmas A., Bulet P.,
RA Aunis D., Metz-Boutigue M.-H.;
RT "Antibacterial and antifungal activities of vasostatin-1, the N-
RT terminal fragment of chromogranin A.";
RL J. Biol. Chem. 275:10745-10753(2000).
RN [15]
RN
RX CARBOHYDRATE-BINDING SITES, PHOSPHORYLATION, AND DISULFIDE BOND.
RX MEDLINE-99459228; PubMed-10527498;
RA Bauer S.H., Zhang X.Y., Van Dongen W., Claeys M., Przybylski M.;
RT "Chromogranin A from bovine adrenal medulla: molecular
RT characterization of glycosylations, phosphorylations, and sequence
RT heterogeneities by mass spectrometry.";
RL Anal. Biochem. 274:69-80(1999).
RN
RX FUNCTION: PANCREASTATIN STRONGLY INHIBITS GLUCOSE INDUCED INSULIN
RX RELEASE FROM THE PANCREAS.
RX FUNCTION: CHROMOSTATIN COMPLETELY INHIBITS CATECHOLAMINE RELEASE
RX FROM CHROMAFFIN CELLS.
RX FUNCTION: CHROMACIN HAS ANTIBACTERIAL ACTIVITY AGAINST MICROCOCCUS
RX LUTEUS.
RX FUNCTION: CATESTATIN INHIBITS CATECHOLAMINE RELEASE FROM
RX CHROMAFFIN CELLS AND NORADRENERGIC NEURONS BY ACTING AS A NON-
RX COMPETITIVE NICOTINIC CHOLINERGIC ANTAGONIST.
RX FUNCTION: VASOSTATIN-1 HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-
RX POSITIVE BACTERIA M.LUTEUS, B.MEGATERIUM, NOT ACTIVE AGAINST GRAM-
RX POSITIVE BACTERIA B.CEREUS, B.SUBTILIS, S.PYROGENES, M.FORTUITUM,
RX S.AUREUS AND L.MONOCYTOGENES AND AGAINST GRAM-NEGATIVE BACTERIA
RX E.COLI, E.CLOACAE, S.TYPHIMURIUM, K.PNEUMONIAE AND P.AURUGINOSA.
RX POSSESSES ANTIFUNGAL ACTIVITY AGAINST N.CRASSA, A.FUMIGATUS,
RX A.BRASSICOLA, N.HEMATOCOCCA, F.CULMORUM AND F.OXYFORUM AND
RX AGAINST S.CEREVISIAE AND C.ALBICANS YEAST. INACTIVE AGAINST
RX T.MENTAGROPHYTES.
RX SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
RX GRANULES.
RX MASS SPECTROMETRY: MW=8584.9; METHOD=MALDI; RANGE=19-94.
RX MISCELLANEOUS: BINDS CALCIUM WITH A LOW-AFFINITY.
RX MISCELLANEOUS: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
RX FAMILY.
RX
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RX or send an email to license@isb-sib.ch).
RX
RX
RX

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DR EMBL; S79270; AAB21297.1; -.
DR EMBL; S79256; AAB21297.1; JOINED.
DR EMBL; S79258; AAB21297.1; JOINED.
DR EMBL; S79260; AAB21297.1; JOINED.
DR EMBL; S79262; AAB21297.1; JOINED.
DR EMBL; S79264; AAB21297.1; JOINED.
DR EMBL; S79266; AAB21297.1; JOINED.
DR EMBL; S79268; AAB21297.1; JOINED.
DR EMBL; X04298; CAA27636.1; -.
DR EMBL; X04298; CAA27636.1; -.
DR EMBL; M16971; AAB30765.1; -.
DR EMBL; U73523; AAC48700.1; -.
DR PIR; A41520; A41520.
DR PIR; A24175; A24175.
DR PIR; A28033; A28033.
DR PDB; 1CFK; 22-MAR-99.
DR GlycoSuiteDB; P05059; -.
DR InterPro; IPR001819; -.
DR InterPro; IPR001990; -.
DR Pfam; PF01271; Granin; 1.
DR PRINTS; PR00659; CHROMOGRANIN.
DR PROSITE; PS00422; GRANINS_1; 1.
DR PROSITE; PS00423; GRANINS_2; 1.
DR Signal; Amidation; Glycoprotein; Calcium-binding; Phosphorylation;
KW Polymorphism; 3D-structure; Antibiotic; Fungicide.
FT SIGNAL 1 18
FT CHAIN 19 449 CHROMOGRANIN A.
FT PEPTIDE 19 94 VASOSTATIN-1.
FT PEPTIDE 142 161 CHROMOSTATIN.
FT PEPTIDE 191 212 CHROMACIN.
FT PEPTIDE 266 312 PANCREASTATIN.
FT PEPTIDE 334 347 WE-14.
FT PEPTIDE 362 382 CAVESTATIN.
FT MOD_RES 99 99 PHOSPHORYLATION (PARTIAL).
FT MOD_RES 142 142 PHOSPHORYLATION (PARTIAL).
FT MOD_RES 191 191 PHOSPHORYLATION.
FT MOD_RES 315 315 PHOSPHORYLATION (PARTIAL).
FT MOD_RES 390 390 PHOSPHORYLATION.

Query Match 9.78; Score 87.5; DB 1; Length 449;
Best Local Similarity 24.48; Pred. No. 6;
Matches 39; Conservative 19; Mismatches 57; Indels 45; Gaps 8;

Qy 6 EFPESEQ---DSSSAERGLSPAGDPSGSGKHQAPGLLMDASHQEQPTSSSHHG 62
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db 138 EKEKSDSDGDRPQASPLGP-----KVEDNQAPG-----EEEPASNAH-- 181

Qy 63 GAGAVEIRSRHSPTAGTDEGMEEPSPRGRSRGAPPNLWAAQRYGRELRMAD--- 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 182 --PLASLPSPKYPGPQAKEDSEGPSQGA-----SREKGLSAEQ--GRTEREEEEK 230

Qy 120 -EFVDSFKKGLPR-----PKSAGTATQMRQSSW 147
| : : : | : | : | : | : | : | : | : | : | : | : | : | :
Db 231 WEEAREKAVPEESPPTAAFKPPPSLGNKETQRAAPGW 270

RESULT 7
SGL_BOVIN
ID_SGL_BOVIN STANDARD; PRT; 646 AA.
AC P23389; O02707;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) [CONTAINS: GAWK
DE PEPTIDE; SECRETOLYTIN].
GN CHGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Adrenal Chromaffin;
RX MEDLINE=91223091; PubMed=2025642;
RA Bauer J.W., Fischer-Colbrie R.;
RT "Primary structure of bovine chromogranin B deduced from cDNA
sequence.";
RL Biochim. Biophys. Acta 1089:124-126(1991).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=97282588; PubMed=9136897;
RA Yoo S.H., Kang Y.K.;
RT "Identification of the secretory vesicle membrane binding region of
chromogranin B.";
RL FEBS Lett. 406:259-262(1997).
[3]
RP SEQUENCE OF 21-646 FROM N.A.
RC TISSUE=Adrenal medulla;
RA Grandy D.K., Leduc R., Makam H., Flanagan T., Diliberto E.J.,
Thomas G., Civelli O., Viveros O.H.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 634-646.
RC TISSUE=Adrenal Chromaffin;
RX MEDLINE=95262699; PubMed=7744058;
RA Strub J.-M., Garcia-Sablone P., Lonning K., Taupenot L., Hubert P.,
van Dorsselaer A., Aunis D., Metz-Boutique M.-H.;
RT "Processing of chromogranin B in bovine adrenal medulla.
Identification of secretolytin, the endogenous C-terminal fragment of
residues 614-626 with antibacterial activity.";
RL Eur. J. Biochem. 229:356-368(1995).
[5]
RP CHARACTERIZATION OF SECRETOLYTIN.
RX MEDLINE=96184581; PubMed=8603705;
RA Strub J.-M., Hubert P., Nullans G., Aunis D., Metz-Boutique M.-H.;
RT "Antibacterial activity of secretolytin, a chromogranin B-derived
peptide (614-626), is correlated with peptide structure.";
RL FEBS Lett. 379:273-278(1996).
CC -1- FUNCTION: SECRETOGRANIN I IS A NEUROENDOCRINE SECRETORY GRANULE
PROTEIN, WHICH MAY BE THE PRECURSOR FOR OTHER BIOLOGICALLY ACTIVE
PEPTIDES. THE 16 PAIRS OF BASIC AA DISTRIBUTED THROUGHOUT ITS
SEQUENCE MAY BE USED AS PROTEOLYTIC CLEAVAGE SITES.
CC -1- FUNCTION: SECRETOLYTIN HAS ANTIBACTERIAL ACTIVITY.
CC -1- SUBCELLULAR LOCATION: NEUROENDOCRINE AND ENDOCRINE SECRETORY
GRANULES.
CC -1- PTM: O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE CHROMOGRANIN / SECRETOGRANIN PROTEIN
FAMILY.
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EMBL; X55027; CAA38846.1; -.
EMBL; U88551; AAC48720.1; -.
EMBL; X55489; CAA39109.1; -.
PIR; S15901; S15901.
InterPro; IPR001819; -.
InterPro; IPR001990; -.
Pfam; PF01271; Granin; 1.
PRINTS; PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS_1; 1.
PROSITE; PS00423; GRANINS_2; 1.
Sulfatation; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT CHAIN 21 646 SECRETOGRANIN I.
FT PEPTIDE 418 484 GAWK PEPTIDE.
FT PEPTIDE 634 646 SECRETOLYTIN.
FT DISULFID 36 57 BY SIMILARITY.
FT MOD_RES 158 158 SULFATATION (POTENTIAL).

```

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FT MOD_RES 315 315 SULFATATION (BY SIMILARITY).
FT CONFLICT 64 64 N -> S (IN REF. 1).
FT CONFLICT 70 70 N -> D (IN REF. 2).
FT CONFLICT 93 98 SEAPGL -> FRSPRAS (IN REF. 3).
FT CONFLICT 181 181 T -> M (IN REF. 2).
FT CONFLICT 261 261 H -> R (IN REF. 2).
FT CONFLICT 386 386 P -> R (IN REF. 2).
FT CONFLICT 481 481 H -> L (IN REF. 3).
FT CONFLICT 597 597 M -> V (IN REF. 2).
FT SEQUENCE 646 AA; 73339 MW; 420DB1178FD9E415 CRC64;

Query Match 9.6%; Score 87; DB 1; Length 646;
Best Local Similarity 27.9%; Pred. No. 9.6;
Matches 36; Conservative 17; Mismatches 52; Indels 24; Gaps 6;

QY 9 PSQEDSSSSNERGLGSPAGDGGSGGKHH--RQAGLLWDASHQEQP--TSSSHHGGA 64
DB 246 PGESEDA-----SPEVDKRRHPRHHGSRP---DRSSQGNPPLEESHVGTG 293
QY 65 GAVEIRSHSSYPAGTDEDEGMGEPPFRGSRSPAPNLAQAQRYGR-----ELRRMA 118
DB 294 NSDEEKARHPAHFALEAGNEYEEVR--RHSAAQAPGDLOGARFGGRGEGHQAALRRPS 351
QY 119 DEFVDSFKK 127
DB 352 EESLEQENK 360
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RESULT 8
ARVC_HUMAN STANDARD; PRT; 962 AA.
AC 000192;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ARMADILLO REPEAT PROTEIN DELETED IN VELO-CARDIO-FACIAL SYNDROME.
GN Arvcf.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (SHORT AND LONG ISOFORMS).
RX MEDLINE=97271559; PubMed=9126485;
RA Sirotkin H., O'Donnell H., Dasgupta R., Halford S., St Jore B.,
RA Puech A., Parimoo S., Morrow B., Skoultschi A., Weissman S.,
RA Scambler P., Kucherlapati R.;
RT "Identification of a new human catenin gene family member (ARVCF) from
RT the region deleted in velo-cardio-facial syndrome.";
RL Genomics 41:75-83(1997).
CC -!- FUNCTION: INVOLVED IN PROTEIN-PROTEIN INTERACTIONS AT ADHERENS
CC JUNCTIONS.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A SHORT FORM AND A LONG FORM
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: FOUND IN ALL THE EXAMINED TISSUES INCLUDING
CC HEART BRAIN, LIVER AND KIDNEY. FOUND AT LOW LEVEL IN LUNG.
CC -!- DISEASE: GENE DELETED IN VELO-CARDIO-FACIAL SYNDROME (VCFS) AND IS
CC HEMIZYGOUS IN ALL VCFS PATIENTS WITH INTERSTITIAL DELETIONS. THIS
CC HEMIZYGOUSITY MAY PLAY A ROLE IN THE ETIOLOGY OF SOME OF THE
CC PHENOTYPES ASSOCIATED WITH VCFS CHARACTERIZED BY A WIDE SPECTRUM
CC PHENOTYPES, INCLUDING CONOTRUNCAL HEART DEFECTS, CLEFT PALATE AND
CC FACIAL DYSMORPHOLOGY.
CC -!- SIMILARITY: BELONGS TO THE BETA-CATENIN FAMILY.
CC -!- SIMILARITY: CONTAINS 10 ARM REPEATS.
CC -----
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CC EMBL; U51269; AAC51202.1; --
DR HSSP; 002248; 2BCT.
DR MIM; 602269; --
DR MIM; 192430; --
DR InterPro; IPR000225; --
DR Pfam; PF00514; Armadillo_seg; 4.
DR PROSITE; PS0176; ARM_REPEAT; 3.
KW Repeat; Coiled coil; Alternative splicing.
FT DOMAIN 8 46 COILED COIL (POTENTIAL).
FT DOMAIN 607 623 NUCLEAR LOCALIZATION (POTENTIAL).
FT DOMAIN 608 611 POLY-ARG.
FT REPEAT 348 387 ARM 1.
FT REPEAT 390 429 ARM 2.
FT REPEAT 433 473 ARM 3.
FT REPEAT 468 508 ARM 4.
FT REPEAT 526 565 ARM 5.
FT REPEAT 575 622 ARM 6.
FT REPEAT 646 686 ARM 7.
FT REPEAT 699 738 ARM 8.
FT REPEAT 739 781 ARM 9.
FT REPEAT 782 826 ARM 10.
FT VARSPPLIC 1 69 MEDCNVHSAASILASVKQEAFERLITRALEQERHRHVALQL
FT ERAQQPGMVSGMGSGQPLPMAQQLVL -> MPALER
FT (IN SHORT ISOFORM).
SQ SEQUENCE 962 AA; 104641 MW; 74A1814A022FF2B1 CRC64;
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Query Match 9.6%; Score 87; DB 1; Length 962;
Best Local Similarity 25.2%; Pred. No. 15;
Matches 39; Conservative 13; Mismatches 55; Indels 48; Gaps 7;

QY 8 EPSEQEDSSSNERGLGSPAGDGGSGGKHHQRAQPCGLLDASHQEQPTSSSHHGAGAV 67
DB 194 EPRDPSYGLSLRGLGNRPFRAGPLGPGP-----GDGCF 227
QY 68 EIRSHSSYPAGTDEDEGMGEPPFRGSRSPAPNLAQAQRYGR--LRRMADEFVDSF 125
DB 228 TLPGRHFAFP-----VGPEPPGGRSL---PERQAEPYGLDDTRSLAAD----- 271
QY 126 KKGLEPR-PKSAGTATQMRQSSS---WTRVFQSWWD 156
DB 272 DEGGPELEPDYGTATRRRPERCGRGLHTRAYEDTAD 306

RESULT 9
HLES_DROME STANDARD; PRT; 1077 AA.
ID HLES_DROME
AC Q02308;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE HAIRLESS PROTEIN.
GN H.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92387549; PubMed=1516831;
RA Bang A.G., Posakony J.W.;
RT "The Drosophila gene Hairless encodes a novel basic protein that
RT controls alternative cell fates in adult sensory organ development.";
RL Genes Dev. 6:1752-1769(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93041287; PubMed=1419850;
RA Maier D., Stumm G., Kuhn K., Preiss A.;
RT "Hairless, a Drosophila gene involved in neural development, encodes
RT a novel, serine rich protein.";
RL Mech. Dev. 38:143-156(1992).
```


RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94268602; PubMed=8208605;
RA Chiba H., Muramatsu M., Nomoto A., Kato H.;
RT "Two human homologues of Saccharomyces cerevisiae SWI2/SNF2 and
DT Drosophila brahma are transcriptional coactivators cooperating with
RT the estrogen receptor and the retinoic acid receptor.";
RL Nucleic Acids Res. 22:1815-1820(1994).
RN [4]
RP SEQUENCE OF 814-1474 FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RX Burkhardt-Schultz K., Gordon L., Dias J., Brower A., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: TRANSCRIPTIONAL COACTIVATOR COOPERATING WITH NUCLEAR
CC HORMONE RECEPTORS TO POTENTIATE TRANSCRIPTIONAL ACTIVATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
CC
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CC
CC EMBL: U29175; ABA04977.1; -
CC EMBL: D26156; BAA05143.1; -
CC EMBL: AC006127; AAC97987.1; -
CC MIM: 603254; -
CC InterPro: IPR000330; -
CC InterPro: IPR001487; -
CC InterPro: IPR001650; -
CC Pfam: PF00176; SNF2_N; 1.
CC Pfam: PF00439; bromodomain; 1.
CC Pfam: PF00271; helicase_C; 1.
CC PRINTS: P00503; BROMODOMAIN.
CC PROSITE: PS00633; BROMODOMAIN_1; 1.
CC PROSITE: PS50014; BROMODOMAIN_2; 1.
CC Transcription regulation; Nuclear protein; Activator; Bromodomain;
KW ATP-binding; Helicase.
FT DOMAIN 578 588 POLY-LYS.
FT DOMAIN 663 672 POLY-GLU.
FT NP_BIND 779 786 ATP (POTENTIAL).
FT SITE 881 884 DEGH BOX.
FT DOMAIN 1360 1364 POLY-GLU.
FT DOMAIN 1477 1547 BROMODOMAIN.
FT DOMAIN 1571 1584 POLY-GLU.
SQ SEQUENCE 1647 AA; 184585 MW; 7B785E7953277F1D CRC64;

Query Match 9.6%; Score 86.5; DB 1; Length 1647;
Best Local Similarity 29.8%; Pred. No. 28;
Matches 31; Conservative 9; Mismatches 55; Indels 9; Gaps 4;
QY 9 PSEQDSSAERGLGSPAGDGGSGKHH---ROAP-GLLWDASHQEQPTSSSHHGA 64
DB 30 PEPGSPGSAHSMWGSP---GPSSAG--HPPTQCGPGYPQDNMQMKPMESMEKCM 84
QY 65 GAVEIKSRHSSYPAGTDEDDGMEEPSPFRGRSRAPNLWAAQ 108
DB 85 SDDPRYNQMGMRSGGHAGMPFPSPMDQHSQGYPSPLGGSE 128
RESULT 12

DMPL_BOVIN .STANDARD; PRT; 510 AA.
ID DMPL_BOVIN AC Q95120;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1 PRECURSOR (DENTIN MATRIX
DE PROTEIN-1) (DMP-1).
GN DMPL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tooth;
RX MEDLINE=97263352; PubMed=9109824;
RA Hirst K.L., Ibaraki-O'Connor K., Young M.F., Dixon M.J.;
RT "Cloning and expression analysis of the bovine dentin matrix acidic
RT phosphoprotein gene.";
RL J. Dent. Res. 76:754-760(1997).
CC -!- FUNCTION: COULD BE INVOLVED IN THE INDUCTION OF MINERALIZATION OF
CC EXTRACELLULAR MATRIX AND IN DENTINOGENESIS.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN FETAL BRAIN, BONE AND TOOTH
CC PARTICULARLY IN ODONTOBLAST, BUT NOT IN AMELOBLAST. NOT EXPRESSED
CC IN LIVER AND SKIN.
CC
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CC
CC EMBL: U47636; AAB09412.1; -
CC Extracellular matrix; Signal.
KW SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 510 DENTIN MATRIX ACIDIC PHOSPHOPROTEIN 1.
FT CARBOHYD 351 351 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 370 370 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 427 427 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SITE 364 366 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 510 AA; 55491 MW; 9BFA9A74F6450865 CRC64;
Query Match 9.4%; Score 85.5; DB 1; Length 510;
Best Local Similarity 25.2%; Pred. No. 9.7;
Matches 29; Conservative 12; Mismatches 35; Indels 39; Gaps 5;
QY 9 PSEQEDSSAERGLGSPAGDGGSGKHHROAPGLLWDASHQ-----HOADESSEEDVLDKPSDS 51
DB 347 PSQENSESQEALHES-RGDNPDNATSHRE-----HOADESSEEDVLDKPSDS 396
QY 52 -----QEQTSSHHGGAGAVEIRSHSSYPAGTDEDDGMEEPSPFRGRSRAP 101
DB 397 ESTSTEQADSESH-----SLRSSEES-PESTEQNSSSQEQAGTQSRSQSP 444
RESULT 13
HERG_HUMAN .STANDARD; PRT; 1159 AA.
ID HERG_HUMAN AC Q12809; O75680;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL HERG (POTASSIUM CHANNEL, VOLTAGE-GATED
DE SUBFAMILY H MEMBER 2) (ETHER-A-GO-GO-RELATED PROTEIN).
GN KCNH2 OR HERG
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RX MEDLINE=94211879; PubMed=8159766;
 RA Warke J.W., Ganetsky B.;
 RT "A family of potassium channel genes related to eag in Drosophila and mammals.";
 RL Hum. Genet. 102:435-439(1998).
 RN [2]
 RP Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT LQT2 CYS-534.
 RX MEDLINE=98260867; PubMed=9600240;
 RA Itoh T., Tanaka T., Nagai R., Kamiya T., Sawayama T., Nakayama T., Tomoike H., Sakurada H., Yazaki Y., Nakamura Y.;
 RA "Genomic organization and mutational analysis of HERG, a gene responsible for familial long QT syndrome.";
 RT Hum. Genet. 102:435-439(1998).
 RL [3]
 RP SEQUENCE OF 27-1159 FROM N.A.
 RA Yang P., Paulussen A., Verhasselt P., Crabbe R., Luyten W., Armstrong M.;
 RA "Analysis of the human HERG gene: intron localisation and identification of a novel inherited mutation associated with long QT.";
 RT Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP VARIANTS LQT2 ASP-470; VAL-561; SER-628 AND 500-ILE--PHE-508 DEL.
 RX MEDLINE=95196272; PubMed=7889573;
 RA Curran M.E., Splawski I., Timothy K.W., Vincent G.M., Green E.D., Keating M.T.;
 RA "A molecular basis for cardiac arrhythmia: HERG mutations cause long QT syndrome.";
 RL Cell 80:795-803(1995).
 RN [5]
 RP VARIANT LQT2 MET-822.
 RX MEDLINE=97071892; PubMed=9914737;
 RA Satler C.A., Walsh E.P., Vesely M.R., Plummer M.H., Ginsburg G.S., Jacob H.J.;
 RA "Novel missense mutation in the cyclic nucleotide-binding domain of HERG causes long QT syndrome.";
 RL Am. J. Med. Genet. 65:27-35(1996).
 RN [6]
 RP VARIANT LQT2 ARG-593.
 RX MEDLINE=96259954; PubMed=8635257;
 RA Benson D.W., MacRae C.A., Vesely M.R., Walsh E.P., Seidman J.G., Seidman C.E., Satler C.A.;
 RA "Missense mutation in the pore region of HERG causes familial long QT syndrome.";
 RL Circulation 93:1791-1795(1996).
 RN [7]
 RP VARIANTS LQT2 ILE-474; VAL-561; HIS-611; VAL-614 AND ALA-630.
 RX MEDLINE=97176600; PubMed=9024139;
 RA Tanaka T., Nagai R., Tomoike H., Takata S., Yano K., Yabuta K., Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y., Nakamura Y.;
 RA "Four novel KVLQT1 and four novel HERG mutations in familial long-QT syndrome.";
 RL Circulation 95:565-567(1997).
 RN [8]
 RP VARIANTS LQT2 CYS-572; ASP-588; VAL-614 AND ALA-630.
 RX MEDLINE=98360095; PubMed=9693036;
 RA Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H., Keating M.T.;
 RA "Genomic structure of three long QT syndrome genes: KVLQT1, HERG, and KCNE1.";
 RL Genomics 51:86-97(1998).
 RN [9]
 RP VARIANTS LQT2 LEU-612; VAL-614; ASP-629; SER-629 AND SER-633.
 RX MEDLINE=98204397; PubMed=9544837;
 RA Satler C.A., Vesely M.R., Duggal P., Ginsburg G.S., Beggs A.H.;
 RT "Multiple different missense mutations in the pore region of HERG in patients with long QT syndrome.";

RL Hum. Genet. 102:265-272(1998).
 RN [10]
 RP VARIANTS LQT2 SER-601.
 RX MEDLINE=98112459; PubMed=9452080;
 RA Akimoto K., Furutani M., Imamura S.-I., Furutani Y., Kasanuki H., Takao A., Momma K., Matsuoka R.;
 RT "Novel missense mutation (G601S) of HERG in a Japanese long QT syndrome family.";
 RL Hum. Mutat. Suppl. 1:S184-S186(1998).
 RN [11]
 RP VARIANTS LQT2 PRO-558; CYS-582; SER-604; MET-613 AND LEU-640.
 RX MEDLINE=99235550; PubMed=10220144;
 RA Jongbloed R.J.E., Wilde A.A.M., Geelen J.L.M.C., Doevendans P., Schaap C., Van Langen I., van Tintelen J.P., Cobben J.M., Beaufort-Krol G.C.M., Geraedts J.P.M., Smeets H.J.M.;
 RT "Novel KCNQ1 and HERG missense mutations in Dutch long-QT families.";
 RL Hum. Mutat. 13:301-310(1999).
 RN [12]
 RP VARIANT LQT2 ARG-572.
 RX MEDLINE=99235552; PubMed=10220146;
 RA Larsen L.A., Christiansen M., Vuust J., Andersen P.S.;
 RT "High-throughput single-strand conformation polymorphism analysis by automated capillary electrophoresis: robust multiplex analysis and pattern-based identification of allelic variants.";
 RL Hum. Mutat. 13:318-327(1999).
 RN [13]
 RP VARIANTS LQT2 L-29; T-33; R-53; Q-56; G-66; R-70; P-78 AND R-86.
 RX MEDLINE=99214568; PubMed=10187793;
 RA Chen J., Zou A., Splawski I., Keating M.T., Sanguinetti M.C.;
 RT "Long QT syndrome-associated mutations in the Per-Arnt-Sim (PAS) domain of HERG potassium channels accelerate channel deactivation.";
 RL J. Biol. Chem. 274:10113-10118(1999).
 RN [14]
 RP VARIANT LQT2 LYS-629.
 RX MEDLINE=99445248; PubMed=10517660;
 RA Yoshida H., Horie M., Otani H., Takano M., Tsuji K., Kubota T., Fukunami M., Sasayama S.;
 RT "Characterization of a novel missense mutation in the pore of HERG in a patient with long QT syndrome.";
 RL J. Cardiovasc. Electrophysiol. 10:1262-1270(1999).
 RN [15]
 RP VARIANT LQT2 ARG-572.
 RX MEDLINE=20197680; PubMed=10735633;
 RA Larsen L.A., Svendsen I.H., Jensen A.M., Kanters J.K., Andersen P.S., Moller M., Sorensen S.A., Sandoe E., Jacobsen J.R., Vuust J., Christiansen M.;
 RT "Long QT syndrome with a high mortality rate caused by a novel G572R missense mutation in KCNH2.";
 RL Clin. Genet. 57:125-130(2000).
 RN [16]
 RP VARIANTS LQT2.
 RX MEDLINE=20432616; PubMed=10973849;
 RA Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori S., Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M., Keating M.T.;
 RT "Spectrum of mutations in long-QT syndrome genes. KVLQT1, HERG, SCN5A, KCNE1, and KCNE2.";
 RL Circulation 102:1178-1185(2000).
 CC -1- FUNCTION: INWARDLY RECTIFYING CARDIAC POTASSIUM (IKR) CHANNEL.
 CC -1- SUBUNIT: MAY ASSEMBLE WITH EITHER MIRP1 OR MINK. COMPLEXES WITH MIRP1 ARE MORE STABLE.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART.
 CC -1- DISEASE DEFECTS IN KCNH2 IS ASSOCIATED WITH LONG QT SYNDROME TYPE 2 (LQT2). THIS DISEASE IS CHARACTERIZED BY A PROLONGED QT SEGMENT ON THE ECG AND POLYMORPHIC VENTRICULAR ARRHYTHMIAS KNOWN AS TORSADES DE POINTES. THESE ARRHYTHMIAS OFTEN OCCUR IN RELATION TO EXERCISE OR EMOTIONAL STRESS AND MAY RESULT IN RECURRENT SYNCOPE, SEIZURES, OR SUDDEN CARDIAC DEATH. DEAFNESS IS OFTEN ASSOCIATED TO THE SYNDROME.
 CC -1- MISCELLANEOUS: IT HAS THE ARCHITECTURAL PLAN OF THE DEPOLARIZATION-ACTIVATED POTASSIUM CHANNEL FAMILY (6 PUTATIVE TRANSMEMBRANE SEGMENTS), YET IT EXHIBITS RECTIFICATION LIKE THAT OF THE INWARD-RECTIFYING POTASSIUM CHANNELS.

CC -!- DATABASE: NAME-LQTSdb; NOTE-KCNH2 mutations page;
CC WWW="http://www.ssi.dk/en/forskning/lqtsdb/herg.htm".

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CC -----
CC EMBL; U04270; AAA62473.1; -
DR EMBL; AB009071; BAA37096.1; JOINED.
DR EMBL; AB009057; BAA37096.1; JOINED.
DR EMBL; AB009058; BAA37096.1; JOINED.
DR EMBL; AB009059; BAA37096.1; JOINED.
DR EMBL; AB009060; BAA37096.1; JOINED.
DR EMBL; AB009061; BAA37096.1; JOINED.
DR EMBL; AB009062; BAA37096.1; JOINED.
DR EMBL; AB009063; BAA37096.1; JOINED.
DR EMBL; AB009064; BAA37096.1; JOINED.
DR EMBL; AB009065; BAA37096.1; JOINED.
DR EMBL; AB009066; BAA37096.1; JOINED.
DR EMBL; AB009067; BAA37096.1; JOINED.
DR EMBL; AB009068; BAA37096.1; JOINED.
DR EMBL; AB009069; BAA37096.1; JOINED.
DR EMBL; AB009070; BAA37096.1; JOINED.
DR EMBL; AB009071; BAA37096.1; JOINED.
DR EMBL; AJ010538; CAA09232.1; -
DR EMBL; AJ010539; CAA09232.1; JOINED.
DR EMBL; AJ010540; CAA09232.1; JOINED.
DR EMBL; AJ010541; CAA09232.1; JOINED.
DR EMBL; AJ010542; CAA09232.1; JOINED.
DR EMBL; AJ010543; CAA09232.1; JOINED.
DR EMBL; AJ010544; CAA09232.1; JOINED.
DR EMBL; AJ010545; CAA09232.1; JOINED.
DR EMBL; AJ010546; CAA09232.1; JOINED.
DR EMBL; AJ010547; CAA09232.1; JOINED.
DR EMBL; AJ010548; CAA09232.1; JOINED.
DR EMBL; AJ010549; CAA09232.1; JOINED.
DR EMBL; AJ010550; CAA09232.1; JOINED.
DR EMBL; AJ010551; CAA09232.1; JOINED.
DR MIM; 152427; -
DR InterPro; IPR000595; -
DR InterPro; IPR001610; -

Query Match 9.4%; Score 85.5; DB 1; Length 1159;
Best Local Similarity 26.6%; Pred No. 23;
Matches 42; Conservative 10; Mismatches 51; Indels 55; Gaps 8;
QY 10 SGOEDSSAERGLGPGAGDPSGSKHHRQAPGLLWDASHQOEQPTSSHHGGAGAVEI 69
Db 899 TEQPGGEVSA---LGPGRAGAPSSRRG-----PGGPWG-----ESPSSG----- 934
QY 70 RSRHSSYPAGTDEDCMGCEPSPFR-----GSRSAAPPNLWAAQRYGRELRRMADEFVD 123
Db 935 -----PSSPESSE-DEGPGRSSPLRLVPFSPRPCEPG-----GPELMDCB----- 978
QY 124 SFKKGLPKPKSAGTATQMRQSSSWTRVFQSWWDRNLGR 161
Db 979 -----KSDTCNPLSCAFSGVSNIFSWGDSRGR 1007

RESULT 14

ID HXA5_MOUSE
AC P09021
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HOMEBOX PROTEIN HOX-A5 (HOX-1.3) (M2).
GN HOXA5 OR HOXA-5 OR HOX-1.3.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=88056292; PubMed=2890554;
RA Odenwald W.F., Taylor C.F., Palmer-Hill F.J., Friedrich V. Jr.,
Rani M., Lazzarini R.A.;
RT "Expression of a homeo domain protein in noncontact-inhibited
RT cultured cells and postmitotic neurons.";
RL Genes Dev. 1:482-496(1987).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=88328807; PubMed=2901335;
RA Fibi M., Zink B., Kessel M., Colberg-Poley A.M., Labelt S.,
Lehrach H., Gruss P.;
RT "Coding sequence and expression of the homeobox gene Hox 1.3.";
RL Development 102:349-359(1988).
RN [3]
RN DNA-BINDING SPECIFICITY.
RX MEDLINE=89232713; PubMed=2565857;
RA Odenwald W.F., Garbern J., Arnheiter H., Tournier-Lasserre E.,
Lazzarini R.A.;
RT "The Hox-1.3 homeo box protein is a sequence-specific DNA-binding
RT phosphoprotein.";
RL Genes Dev. 3:158-172(1989).
RN [4]
RN CHARACTERIZATION.
RX MEDLINE=96205869; PubMed=8635464;
RA Zhao J.J., Lazzarini R.A., Pick L.;
RT "Functional dissection of the mouse Hox-a5 gene.";
RL EMBO J. 15:1313-1322(1996).
CC -!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC ALSO BINDS TO ITS OWN PROMOTER. BINDS SPECIFICALLY TO THE MOTIF:
CC 5'-CYNNATTA[TG]Y-3'.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS AND IN ADULT
CC KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEBOX PROTEINS.
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CC or send an email to license@isb-sib.ch).

Query Match 9.4%; Score 85; DB 1; Length 270;

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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:03:21 ; Search time 35.13 Seconds
(without alignments)
632.714 Million cell updates/sec

Title: 09-580523-lb
Perfect score: 905
Sequence: 1 MFQIPEFPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	902	99.7	168	4	014803
2	633.5	70.0	205	11	035147
3	633.5	70.0	205	11	070256
4	443	49.0	220	11	09JHX1
5	204.5	22.6	95	13	Q919N2
6	100	11.0	272	4	Q9NS37
7	100	11.0	608	14	Q9Q5K9
8	98.5	10.9	569	13	Q9DF20
9	98.5	10.9	923	5	Q9NKN4
10	98	10.8	355	2	Q9RDL8
11	96.5	10.7	867	10	Q9FVZ6
12	96.5	10.7	980	4	Q9Y387
13	96.5	10.7	2506	4	Q9NS88
14	96	10.6	2472	4	Q9NS89
15	94.5	10.4	1398	11	Q9Q000
16	94.5	10.4	1729	5	Q25734
17	94	10.4	1146	5	Q9NQ09
18	93.5	10.3	549	4	Q9H0B9
19	93.5	10.3	1203	4	Q9UPQ9

20	93	10.3	903	4	Q9UPX1
21	93	10.3	1300	14	036421
22	92.5	10.2	1082	11	Q9EPU2
23	92	10.2	622	4	Q9NTE2
24	92	10.2	701	4	Q9NTP8
25	92	10.2	803	4	Q9ULK9
26	91.5	10.1	1714	10	Q9FMM3
27	91	10.1	414	11	Q9ERU8
28	91	10.1	474	5	Q9VA96
29	91	10.1	670	5	Q9NEL2
30	90.5	10.0	393	11	Q9H719
31	90.5	10.0	393	11	P70429
32	90	9.9	990	4	Q15206
33	90	9.9	1218	4	Q05331
34	89.5	9.9	336	14	Q98321
35	89	9.8	362	4	Q95884
36	89	9.8	416	4	Q9UI08
37	89	9.8	418	4	Q9UIC2
38	88.5	9.8	651	4	Q9NXI9
39	88.5	9.8	667	14	Q9PY84
40	88.5	9.8	809	5	Q9NAN8
41	88.5	9.8	845	4	Q9HAU3
42	88.5	9.8	947	10	Q9LWJ9
43	88.5	9.8	2715	5	Q61603
44	88	9.7	222	4	Q9UF25
45	88	9.7	462	6	Q97643

ALIGNMENTS

RESULT 1

O14803 ID O14803 PRELIMINARY; PRT; 168 AA.
AC O14803;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).
GN BAD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97083574; PubMed=8929532;
RA Wang H.G., Rapp U.R., Reed J.C.;
RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
RL Cell 87:629-638(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Takayama S., Reed J.C.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Otilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G.,
RA Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T.;
RL J. Biol. Chem. 0:0-0(1997).
DR EMBL; AF021792; AAB72092.1; -;
DR EMBL; AF031523; AAB88124.1; -;
FT NON_TER 1
SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 99.7%; Score 902; DB 4; Length 168;
Best Local Similarity 99.4%; Pred. No. 6.6e-75;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFPSEQEDSSAERGLGSPAGDGGSGKHHRRQAPGLLWDASHOQEPTSSSH 60
Db 1 MFQIPEFPSEQEDSSAERGLGSPAGDGGSGKHHRRQAPGLLWDASHOQEPTSSSH 60

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QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEEPPFRGSRSPAPNLWAAQRYGRELRRMADE 120
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Db 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEEPPFRGSRSPAPNLWAAQRYGRELRRMSDE 120
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||

RESULT 2
O35147
ID O35147 PRELIMINARY; PRT; 205 AA.
AC O35147;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER.
GN BAD.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC TISSUE=OVARY;
RX MEDLINE=98034386; PubMed=9369453;
RA Hsu S.Y., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
DR EMBL; AF003523; AAC53374.1; -.
SQ SEQUENCE 205 AA; 22468 MW; 04DD3EBA03B11168 CRC64;
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Query Match 70.0%; Score 633.5; DB 11; Length 205;
Best Local Similarity 74.6%; Pred. No. 2.3e-50;
Matches 126; Conservative 12; Mismatches 24; Indels 7; Gaps 4;

QY 1 MFQIPEFESEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
Db 43 MFQIPEFESEQEDASTDRGLGSLTEQDQ---GPY--LAPGLLGSIVQQQPGQAANNS 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEGMEGEEPPFRGSRSPAPNLWAAQRYGRELRRMAD 119
|||||
Db 98 HGGAGTMTETRSRHSYPAGTDEGMEELSPFRGSRSPAPNLWAAQRYGRELRRMSD 157
|||||

QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 158 EFGSP-KGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSGTSPQ 205
|||||
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RESULT 3
O70256
ID O70256 PRELIMINARY; PRT; 205 AA.
AC O70256;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
DE ALPHA).
GN BAD OR BAD-ALPHA.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC TISSUE=BRAIN;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator Bad in
RT the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
```

```
RN [2]
SEQUENCE FROM N.A.
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031227; AAC15100.1; -.
DR EMBL; AF279910; AAF91427.1; -.
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 70.0%; Score 633.5; DB 11; Length 205;
Best Local Similarity 74.6%; Pred. No. 2.3e-50;
Matches 126; Conservative 12; Mismatches 24; Indels 7; Gaps 4;

QY 1 MFQIPEFESEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
Db 43 MFQIPEFESEQEDASTDRGLGSLTEQDQ---GPY--LAPGLLGSIVQQQPGQAANNS 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEGMEGEEPPFRGSRSPAPNLWAAQRYGRELRRMAD 119
|||||
Db 98 HGGAGTMTETRSRHSYPAGTDEGMEELSPFRGSRSPAPNLWAAQRYGRELRRMSD 157
|||||

QY 120 EFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
Db 158 EFGSP-KGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSGTSPQ 205
|||||

RESULT 4
Q9JHX1
ID Q9JHX1 PRELIMINARY; PRT; 220 AA.
AC Q9JHX1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.
GN BAD-BETA.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC TISSUE=OVARY;
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279911; AAF91428.1; -.
SQ SEQUENCE 220 AA; 24278 MW; E27BCD7C969E90F CRC64;
```

```
Query Match 49.0%; Score 443; DB 11; Length 220;
Best Local Similarity 71.7%; Pred. No. 5.5e-33;
Matches 91; Conservative 9; Mismatches 21; Indels 6; Gaps 3;

QY 1 MFQIPEFESEQEDSSAERGLGSPAGDGPSSGKHHRQAPGLLWDASHQOE-QPTSSS 59
|||||
Db 43 MFQIPEFESEQEDASTDRGLGSLTEQDQ---GPY--LAPGLLGSIVQQQPGQAANNS 97
|||||

QY 60 HGGAGAVEIRSRHSSYPAGTDEGMEGEEPPFRGSRSPAPNLWAAQRYGRELRRMAD 119
|||||
Db 98 HGGAGTMTETRSRHSYPAGTDEGMEELSPFRGSRSPAPNLWAAQRYGRELRRMSD 157
|||||

QY 120 EFVDSFK 126
Db 158 EFGSPK 164
|||||

RESULT 5
Q9I9N2
ID Q9I9N2 PRELIMINARY; PRT; 95 AA.
AC Q9I9N2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
```

01-OCT-2000 (TReMBLrel. 15, Last sequence update)
01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE BAD (FRAGMENT).
GN BAD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20337392; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with Homology to Mammalian Apoptosis Regulators Identified in
RT zebrafish";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL: AF231017; AAF66962.1; -;
FT NON_TER 1
SQ SEQUENCE 95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;

Query Match 22.68; Score 204.5; DB 13; Length 95;
Best Local Similarity 48.98; Pred. No. 1.2e-11;
Matches 44; Conservative 11; Mismatches 24; Indels 11; Gaps 3;

QY 83 DEGMGEPP-----SPFRGRSRAPPNLWAAQRYGRELRRMADEFVDSFKKGLPRPKSAGTA 138
DB 13 ETGVAEDPHMLGDFRPRRSAPPALWAAKKYGOOLRRMSDE----FDKMKRVKSAGTA 68
QY 139 TOMROSSWTRVFOSWDRNLGRGSSAPSQ 168
DB 69 ROMSQSPSWLAFL---WSHKESDAESRPAE 95

RESULT 6
Q9NS37 ID Q9NS37 PRELIMINARY; PRT; 272 AA.
AC Q9NS37;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE HCF-BINDING TRANSCRIPTION FACTOR ZHANGFEI.
GN ZF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330366; PubMed=10871379;
RA Lu R., Misra V.;
RT "Zhangfei: a second cellular protein interacts with herpes simplex
RT virus accessory factor HCF in a manner similar to Human and VP16";
RL Nucleic Acids Res. 28:2446-2454(2000).
DR EMBL: AF039942; AAD28325.1; -;
DR InterPro: IPR001871; -;
DR Pfam: PF00170; bZIP: 1.
DR SMART: SM00338; BRLZ: 1.
SQ SEQUENCE 272 AA; 28859 MW; 81F94B438F0702BF CRC64;

Query Match 11.08; Score 100; DB 4; Length 272;
Best Local Similarity 28.78; Pred. No. 0.12;
Matches 41; Conservative 13; Mismatches 67; Indels 22; Gaps 5;

QY 10 SEQEDSSAERGLGSPAGDPGSGGKHRRQAPGLLWDASHQOQPTSSSHHGAGAVEI 69
DB 92 SSSSDSGSAEKRRKRRKSGGGGGGGGNDNQA-----ATKSPKRAAAAAARL 138
QY 70 -RSRSHSSYPAGTEDD-EGMGEEPPFRGRSRAPPNLWAAQRYGRELRR-MADEFVDSFK 126
DB 139 NLRKKKTYVMGSLRVGLAAENQELRAENRELKRVQALQESRYLRAVLANE----- 192

QY 127 KGLPRPKSAGTATQMROSSSWTR 149
DB 193 TGLARLLSRLSGVGLRLTSLFR 215

RESULT 7
Q9Q5K9 ID Q9Q5K9 PRELIMINARY; PRT; 608 AA.
AC Q9Q5K9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE NTR.
OS Herpesvirus papio.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BABOON LYMPHOCRYPTOVIRUS BA65;
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
RA Hayward G.S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF200364; AAF23950.1; -;
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 11.08; Score 100; DB 14; Length 608;
Best Local Similarity 33.38; Pred. No. 0.27;
Matches 37; Conservative 7; Mismatches 55; Indels 12; Gaps 3;

QY 9 PSEQEDSSAERGLGSPAGDPGSGGKHRRQAPGLLWDASHQOQPTSSSHHG---GA 64
DB 502 PTERRRCSAQRGHPGPGAGORPSGPTGGHAAACAPGPRPTERRRCSAQRGHPGGA 561
QY 65 GAVEIRSRHSSYPAGTEDD-EGMGEEPPFRGRSRAPPNLWAAQRYGRELRR 115
DB 562 G-----QRPSGPTGGHAAACAPGAPGPPNPERGSGPADPP---AATRLPLEPR 604

RESULT 8
Q9DF20 ID Q9DF20 PRELIMINARY; PRT; 569 AA.
AC Q9DF20;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE KH DOMAIN CONTAINING RNA-BINDING PROTEIN FMRL.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20501263; PubMed=11046149;
RA Wan L., Dockendorff T.C., Jongens T.A., Dreyfuss G.;
RT "Characterization of dFMR1, a Drosophila melanogaster Homolog of the
RT Fragile X Mental Retardation Protein";
RL Mol. Cell. Biol. 20:8536-8547(2000).
DR EMBL: AF305882; AAG22046.1; -;
SQ SEQUENCE 569 AA; 63906 MW; 2E66A0689F7EDFB5 CRC64;

Query Match 10.98; Score 98.5; DB 13; Length 569;
Best Local Similarity 32.38; Pred. No. 0.34;
Matches 31; Conservative 8; Mismatches 42; Indels 15; Gaps 3;

QY 11 EQEDSSAERGLGSPAGDPGSGGKHRRQAP---GLLWDASHQOQPTSSSHHGAGAGA 66
DB 391 EKEKSFMDNMGSPRGKGKFGRGRRRGPTLASGNNSNASNASE--TESDH----- 442
QY 67 VEIRSRHSSYPAGTEDD-EGMGEEPPFRGRSRAPP 102

RESULT 15

Query Match 10.48; Score 94.5; DB 11; Length 1398;

Best Local Similarity	25.9%; Pred. NO. 2;		
Matches	37; Conservative	12; Mismatches	59; Indels
Gaps	6;		

Search completed: October 9, 2001, 16:03:21
Job time: 306 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:59:14 ; Search time 33.29 Seconds
(without alignments)
305.943 Million cell updates/sec

Title: 09-580523-lb

Perfect score: 905

Sequence: 1 MFQIFEPFSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
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14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
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17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
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19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	99.7	168	19	AAW5779 Human Bcl-xL/Bcl-2
2	902	99.7	168	21	AA13512 Human cell prolif
3	902	99.7	168	22	AA13512 Human cell prolif
4	902	99.7	168	22	AA13512 Human cell prolif
5	748	82.7	166	18	AA13512 Human cell prolif
6	646	71.4	162	22	AA13512 Human cell prolif
7	646	71.4	204	17	AA13512 Human cell prolif
8	646	71.4	204	19	AA13512 Human cell prolif
9	646	71.4	204	19	AA13512 Human cell prolif
10	646	71.4	204	22	AA13512 Human cell prolif
11	643	71.0	204	19	AA13512 Human cell prolif

12	640	70.7	204	19	AAW61316	Mutant BCL-XL/BCL-
13	640	70.7	204	19	AAW61318	Mutant BCL-XL/BCL-
14	311	34.4	59	19	AAW61319	Mutant BCL-XL/BCL-
15	311	34.4	59	19	AAW61320	Mutant BCL-XL/BCL-
16	308	34.0	59	19	AAW61321	Mutant BCL-XL/BCL-
17	305	33.7	56	21	AAW61322	Mutant BCL-XL/BCL-
18	159	17.6	56	21	AAW61322	Mutant BCL-XL/BCL-
19	130	14.4	26	21	AAW61321	Mammalian Bad Bcl-
20	130	14.4	26	22	AAW61321	Mammalian Bad Bcl-
21	117.5	13.0	27	21	AAW61321	BAD BH3 consensus
22	113	12.5	27	21	AAW61321	Bcl2 polypeptide B
23	111	12.3	26	21	AAW61321	Bcl-x(L)/bcl-2 ass
24	111	12.3	26	21	AAW61321	Bcl2 polypeptide B
25	111	12.3	27	21	AAW61321	Bcl2 polypeptide B
26	111	12.3	28	21	AAW61321	Bcl2 polypeptide B
27	97	10.7	2510	16	AAW61321	Human neuronal cal
28	97	10.7	2510	16	AAW61321	Human neuronal cal
29	96.5	10.7	1182	20	AAW61321	Human SCA6 protein
30	95.5	10.6	395	21	AAW61321	Human cytoskeleton
31	94.5	10.4	1447	20	AAW61321	Murine PCIP protei
32	94.5	10.4	1726	17	AAW61321	Truncated Plasmodi
33	94	10.4	1931	13	AAW61321	Human calcium chan
34	93.5	10.3	549	21	AAW61321	A human proliferat
35	90.5	10.0	393	19	AAW61321	Murine Ena-Vasp li
36	90	9.9	434	17	AAW61321	Peptide fragment o
37	90	9.9	434	21	AAW61321	Human N-type calci
38	90	9.9	2237	16	AAW61321	Human neuronal cal
39	90	9.9	2237	19	AAW61321	Human calcium chan
40	90	9.9	2237	21	AAW61321	Human calcium chan
41	90	9.9	2337	19	AAW61321	Human calcium chan
42	90	9.9	2339	14	AAW61321	Sequence of the al
43	90	9.9	2339	16	AAW61321	Human neuronal cal
44	90	9.9	2339	19	AAW61321	Human calcium chan
45	90	9.9	2339	21	AAW61321	Human calcium chan

ALIGNMENTS

RESULT 1

AAW5779 AAW5779 standard; Protein; 168 AA.

XX AC AAW5779;

XX DT 17-JUL-1998 (first entry)

XX DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX DE Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;

XX KW programmed cell death; apoptosis.

XX OS Homo sapiens.

XX PN WO9812328-A2.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-US16991.

XX PR 20-SEP-1996; 96US-0717123.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Horne WA, Oltersdorf T;

XX DR WPI; 1998-217267/19.

XX DR N-PSDB; AAV25877.

XX PT Bad gene mediating apoptosis - used to develop products for treating

XX PT e.g. neurodegenerative disease, cancers or autoimmune disease

XX PS Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-XL/Bcl-2 associated
 CC death promoting polypeptide, Bad, the binding of which to Bcl-XL
 CC results in the induction of programmed cell death, i.e. apoptosis.
 CC Bad can be used in screening assays for compounds to treat or
 CC prevent diseases characterised by apoptotic cell death, such as
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
 CC aplastic anaemia and ischaemic injury including myocardial
 CC infarction, stroke and reperfusion injury. Assays can also be
 CC used to obtain apoptosis enhancing compounds to treat or prevent
 CC diseases characterised by the loss of apoptotic cell death, such as
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated
 CC glomerulonephritis and viral infections, e.g. herpesvirus,
 CC poxvirus or adenovirus infection. Bad can also be used for
 CC detection and diagnosis.
 CC
 XX Sequence 168 AA;
 SQ

Query Match 99.7%; Score 902; DB 19; Length 168;
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDPSGSGKHHRQAPGLLWDASHHQEQPTSSSH 60
 DB 1 mfiqipefepseqedsssaerglpsagdgpsgkhhrqapglldashhqqeqptsssh 60
 QY 61 HGAGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRMADE 120
 DB 61 hgagagaveirsrhssypagteddegmgeepsprgrsrsappnlwaaqrygrelrmsde 120
 QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWDRNLGRGSSAPSQ 168
 DB 121 fvdskkglprpksagtatqmrqssswtrvfqswdrnlgrgssapsq 168

RESULT 2
 AAB13512
 ID AAB13512 standard; protein; 168 AA.
 AC AAB13512;
 XX
 XX
 DT 02-NOV-2000 (first entry)
 XX
 XX Human cell proliferation protein APOP-1.
 DE
 XX Human; cell proliferation; APOP-1; cancer; inflammation; infection;
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.
 KW
 XX Homo sapiens.
 OS
 XX US6080847-A.
 PN
 XX 27-JUN-2000.
 PD
 XX
 XX 04-DEC-1997; 97US-0985335.
 PF
 XX
 XX 04-DEC-1997; 97US-0985335.
 PR
 XX
 XX (INCY-) INCYTE PHARM INC.
 PA
 XX Corley NC, Hillman JL, Yue H, Lal P, Shah P;
 PI
 XX WPI; 2000-451230/39.
 DR
 XX N-PSDB; AAA63332.
 DR
 XX Novel polynucleotide and polypeptide sequences of proteins associated
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.
 PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease.
 PT
 XX

PS Example 8; Fig 1; 58pp; English.
 XX

The present sequence is the human APOP-1 protein. This protein, which
 CC shares structural and chemical homology with Bcl-2, is involved in cell
 CC proliferation. Its coding sequence was isolated by screening a synovial
 CC tissue cDNA library using a computer search for amino acid sequence
 CC alignments. The gene and protein can be used in the treatment of various
 CC cancers, disorders with associated inflammation such as Addison's
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
 CC of cancer, haemodialysis and extracorporeal circulation, infections,
 CC trauma, disorders with associated apoptosis including AIDS and other
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
 CC such as myocardial infarction, and wasting diseases including cachexia.
 CC
 XX Sequence 168 AA;
 SQ

Query Match 99.7%; Score 902; DB 21; Length 168;
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPFEPSEQEDSSAERGLGPGAGDPSGSGKHHRQAPGLLWDASHHQEQPTSSSH 60
 DB 1 mfiqipefepseqedsssaerglpsagdgpsgkhhrqapglldashhqqeqptsssh 60
 QY 61 HGAGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLWAAQRYGRELRMADE 120
 DB 61 hgagagaveirsrhssypagteddegmgeepsprgrsrsappnlwaaqrygrelrmsde 120
 QY 121 FVDSFKKGLPRPKSAGTATQMROSSSWTRVFQSWDRNLGRGSSAPSQ 168
 DB 121 fvdskkglprpksagtatqmrqssswtrvfqswdrnlgrgssapsq 168

RESULT 3
 AAB70368
 ID AAB70368 standard; protein; 168 AA.
 XX
 AC AAB70368;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 XX Human BAD mutant amino acid sequence SEQ ID NO:1.
 DE
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
 KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 XX WO200110888-A1.
 PN
 XX 15-FEB-2001.
 PD
 XX
 XX 30-MAY-2000; 2000WO-US11864.
 PF
 XX
 XX 28-MAY-1999; 99US-0136783.
 PR
 XX (APOP-) APOPTOSIS TECHNOLOGY INC.
 PA
 XX Zhou X;
 PI
 XX

DR WPI; 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Claim 1; Page 147; 157pp; English.
 XX
 CC The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
 CC neurotropic, antiischaemic, vulnerary, cytostatic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed human BAD mutant amino acid sequence from the present invention.
 XX
 SQ Sequence 168 AA;

Query Match 99.7%; Score 902; DB 22; Length 168;
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFQIPEFPESEQEDSSAERGLGSPAGDGGSGKHHRQAPGLLWDASHQEQPTSSSH 60
 Db 1 mfiqipefepseqedsssaerglgpsagdgpsgskhrrqapglldashhqeptsssh 60
 Qy 61 HGGAGAVIRSRHSYPAGTDEGCMGEEPSPFRCRSRAPPNLWAAQRYGRELRRMADE 120
 Db 61 hggagavairsrhsypagtdedgmgeepsfgrsrsappnlwaaqrygrellrmsde 120
 Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRLNLRGSSAPSQ 168
 Db 121 fvdskfkgllprpkasagtatmrqssswtrvfgswdrnlrgssapsq 168

RESULT 4
 AAB48287
 ID AAB48287 standard; protein; 168 AA.
 AC AAB48287;
 XX
 DT 02-APR-2001 (first entry)
 XX Human Bad protein.
 DE
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytostatic.
 XX
 OS Homo sapiens.
 XX WO200075184-A1.
 PN 14-DEC-2000.
 XX
 PF 05-JUN-2000; 2000WO-USI5449.
 XX
 PR 04-JUN-1999; 99US-0137494.
 XX
 PA (UYVA) UNIV YALE.

XX Zhang H, Tsvetkov LM, Kondo T;
 PI WPI; 2001-061703/07.
 DR N-PSDB; AAC84599.
 DR
 XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins -
 XX
 PS Claim 5; Page 102-103; 162pp; English.
 XX
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
 CC cullin/CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours.
 XX
 SQ Sequence 168 AA;
 Query Match 99.7%; Score 902; DB 22; Length 168;
 Best Local Similarity 99.4%; Pred. No. 7.2e-88;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MFQIPEFPESEQEDSSAERGLGSPAGDGGSGKHHRQAPGLLWDASHQEQPTSSSH 60
 Db 1 mfiqipefepseqedsssaerglgpsagdgpsgskhrrqapglldashhqeptsssh 60
 Qy 61 HGGAGAVIRSRHSYPAGTDEGCMGEEPSPFRCRSRAPPNLWAAQRYGRELRRMADE 120
 Db 61 hggagavairsrhsypagtdedgmgeepsfgrsrsappnlwaaqrygrellrmsde 120
 Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRLNLRGSSAPSQ 168
 Db 121 fvdskfkgllprpkasagtatmrqssswtrvfgswdrnlrgssapsq 168

RESULT 5
 AAW32476
 ID AAW32476 standard; Protein; 166 AA.
 XX
 AC AAW32476;
 XX
 DT 15-JAN-1998 (first entry)
 XX BBC6 protein for regulating cell death.
 DE
 DE BBC6 gene; cell death; cell cycle; Bcl2; human.
 KW
 KW Homo sapiens.
 OS
 XX US5663316-A.
 PN
 XX 02-SEP-1997.
 PD
 XX 18-JUN-1996; 96US-0665617.
 PF
 XX 18-JUN-1996; 96US-0665617.
 PR
 XX (CLON-) CLONTECH LAB INC.
 PA
 XX Xudong Y;
 PI
 XX WPI; 1997-447980/41.
 DR N-PSDB; AAT91561.
 DR
 XX Isolated BBC6 gene - encodes a protein that regulates cell death
 PT through interaction with Bcl-2

XX PS Claim 1; Column 11-12; 7pp; English.

XX CC The present sequence represents a protein of 166 amino acids. The

CC sequence is disclosed as a protein called BBC6 which regulates

CC cell death through interaction with Bcl-2. The DNA may be used for the

CC production of the recombinant protein, which can be used in unspecified

CC therapeutic or diagnostic procedures, as a molecular weight marker, and

CC to raise antibodies that can be used in unspecified diagnostic or

CC therapeutic applications and to reduce or eliminate the biological

CC activity of the BBC6 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 82.7%; Score 748; DB 18; Length 166;

Best Local Similarity 83.4%; Pred. No. 1.5e-71;

Matches 146; Conservative 4; Mismatches 9; Indels 16; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPG-----LLWDASHQOE 53

Db 1 mfgipefepseqedsssaerg-wrspagtp-----qapasliarpqvlwdashqoe 51

QY 54 QPTSSSHHGAGAVEIRSRHSSYPAGTDEDEGMGEPSFGRSRSAPPNLWAAQRYGRE 113

Db 52 qptssshhgagaveirsrhssypagtdedegmgeepsfgrararppnlwaaqrygre 111

QY 114 LRRMADEEVDSFKKGLPRPKSAGTATQMRQSSSWTRVFSQWMDNLGRGSSAPSQ 168

Db 112 lrmsdevfdsfkglprpksagatqmrqssswtrvfqswmdnlgrgtaapsq 166

RESULT 6

AAB70370

ID AAB70370 standard; protein; 162 AA.

XX AC AAB70370;

XX DT 02-MAY-2001 (first entry)

XX DE Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX KW Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

KW immunostimulant; neuroprotective; nontropic; antischismatic; vulnary;

KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW immunodeficiency disease; neurodegenerative disease; viral infection;

KW ischaemic cell death; reperfusion cell death; arthritis; infertility;

KW lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Mus musculus.

OS Synthetic.

XX WO200110888-A1.

XX PD 15-FEB-2001.

XX PF 30-MAY-2000; 2000WO-US11864.

XX PR 28-MAY-1999; 99US-0136783.

XX PA (APOB-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX WPI; 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,

PT useful for screening for candidate compounds which induce or inhibit

PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or

PT Ser113 -

XX PS Claim 7; Page 148-149; 157pp; English.

XX CC The present invention describes an isolated or synthetic polypeptide

CC (1) comprising a less than full length amino acid sequence of a mutant

CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its

CC fragment, which contains amino acid substitutions at Ser118 of a human

CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine

CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,

CC nontropic, antischismatic, vulnary, cytostatic, antiviral,

CC antiarthritic, antiinflammatory and immunosuppressive activities, and

CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and

CC polynucleotides can be used for screening candidate compounds and drugs

CC for activity that promote cell survival or apoptosis. Other uses include

CC inducing or inhibiting apoptosis in a cell. Candidate compounds

CC identified and (mutant) BAD polypeptides are useful in treating

CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell

CC death, reperfusion cell death, wound healing, cancer, viral infections,

CC lymphoproliferative conditions, arthritis, infertility, inflammation and

CC autoimmune diseases. The present sequence represents a specifically

CC claimed shorter murine BAD mutant amino acid sequence from the present

CC invention.

XX SQ Sequence 162 AA;

Query Match 71.4%; Score 646; DB 22; Length 162;

Best Local Similarity 75.0%; Pred. No. 9e-61;

Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLWDASHQOEQPTSSSH 60

Db 1 mfgipefepseqedssatdrglpsitedqp---gpy--lapglgslhqqggraatnsh 55

QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPSFGRSRSAPPNLWAAQRYGRELRMADE 120

Db 56 hggagaveirsrhssypagtdedegmeeisfgrsrsappnlwaaqrygrelrmsde 115

QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFSQWMDNLGRGSSAPSQ 168

Db 116 fegsf-kglprpksagatqmrqsgwtrliqswdnlgrkggstpsq 162

RESULT 7

AAR95168

ID AAR95168 standard; Protein; 204 AA.

XX AC AAR95168;

XX DT 06-JAN-1997 (first entry)

XX DE bcl-x(L)/bcl-2 associated death promoter protein.

XX KW Epitope: murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;

KW polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;

KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

KW neurodegenerative disease; senescence; ischaemia; neoplasia.

XX OS Mus musculus.

OS Location/Qualifiers

FT Key 147..149

FT Region /note= "BH1 conserved amino acids"

FT Region 191..192

FT /note= "BH2 conserved amino acids"

FT Domain 38..61

FT /note= "PEST sequence"

FT Domain 111..130

FT /note= "PEST sequence"

XX WO9613614-A1.

XX PD 09-MAY-1996.

XX PF 31-OCT-1995; 95WO-US14246.

```

XX 31-OCT-1994; 94US-0333565.
XX (UNIW ) UNIV WASHINGTON.
XX Korsmeyer SJ;
XX WPI; 1996-251465/25.
XX DR N-PSDB; AAT29479.
XX
XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
XX useful to treat neoplasia and apoptosis and to identify agents
XX inhibiting its binding to bcl-2 or bcl-x(L) to form heterodimers
XX
XX Claim 3; Fig 1; 130pp; English.
XX
XX This sequence represents the murine bcl-x(L)/bcl-2 associated death
XX promoter (Bad) gene. Bad is a 22.1 kD protein which interacts with
XX bcl-2 and bcl-x proteins and regulates cell death. It has homology
XX to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad
XX has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
XX assays and in vivo in mammalian cells. Overexpressed Bad counters the
XX death inhibitory activity of bcl-x(L), but is much less effective at
XX countering the death inhibitory activity of bcl-2. Bad expression can
XX accelerate apoptotic cell death induced by cytokine deprivation in an
XX IL-3 dependent cell line expressing bcl-x(L), and its also counters the
XX death repressor activity of bcl-x(L). Bad competes with Bax for binding
XX to bcl-x(L). Bad may be used to identify agents which inhibit its
XX binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
XX used to treat neurodegenerative diseases, immunodeficiency diseases,
XX e.g. AIDS, senescence or ischaemia.
XX
XX Sequence 204 AA;
XX
XX Query Match 71.4%; Score 646; DB 17; Length 204;
XX Best Local Similarity 75.0%; Pred. No. 1.2e-60;
XX Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps
XX
XX QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSGSGKHHRQAPCLLWDASHQEQPTSSSH 60
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 43 mfiqefepseqedasaatdrglpsitedqp---gpy--lapllgslnhqggraatsh 97
XX
XX QY 61 HGAGAVEINRSHSSYPAGTEDEGMEGPEPFRGRSRGSRAPNLWAAQRYGRELRRMADE 120
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 98 hggagametrshrshssypagteedegmeeelspfgrsrappnlwaaqrgrelrrmsde 157
XX
XX QY 121 FVDSFFKGLPRPKSACTATQMRQSSSWTRVFQSWDRNLGRCSSAPSQ 168
XX Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 158 fegsf-kglprpkrsagatqmrqsagwtrliqswdrnlkggsgtpsq 204
XX
XX RESULT 8
XX AAW61315
XX ID AAW61315 standard; Protein; 204 AA.
XX XX
XX AC AAW61315;
XX XX
XX DT
XX DT
XX XX
XX DE Murine BCL-XL/BCL-2 associated cell death regulator.
XX
XX KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein
XX KW serine substituted mutant; apoptosis; cancer; viral infection.
XX OS Mus sp.
XX XX
XX W09817682-A1.
XX PN
XX PD 30-APR-1998.
XX XX
XX PF 17-OCT-1997; 97WO-US19175.
XX

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KW cancer, viral infection; lymphoproliferative condition; arthritis;
KW inflammation; autoimmune diseases.
OS Mus sp.
PN WO9809643-A1.
PD 12-MAR-1998.
XX 09-SEP-1997; 97WO-US15871.
XX 09-SEP-1996; 96US-0707868.
PR (UNIW) UNIV WASHINGTON.
XX Kormeyer SJ;
PI WPI; 1998-207049/18.
XX Serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
PT polypeptide - useful for modulation of apoptosis associated with,
PT e.g. cancer and immunodeficiency diseases
XX Claim 3; Fig 8: 61pp; English.
PS This sequence represents a novel serine-phosphorylated protein, BAD
XX (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
CC phosphorylated in a post-translational modification and allows binding
CC to the 14-3-3 protein which is a signal transduction regulator.
CC Modulators of phosphorylated BAD, which act through inhibition/activation
CC of a phosphoserine phosphatase, are useful for preventing/treating
CC increased/decreased apoptosis in a cell. The increased apoptosis may
CC result from immunodeficiency diseases, senescence, neurodegenerative
CC disease, ischaemic cell death, reperfusion cell death, infertility and
CC wound-healing. Decreased apoptosis may result from cancer, viral
CC infection, lymphoproliferative conditions, arthritis, infertility,
CC inflammation and autoimmune diseases. Measuring the amount of
CC phosphorylated compared to unphosphorylated BAD polypeptide and/or total
CC BAD in a cell is useful for determining the apoptotic state of a cell.
XX Sequence 204 AA;
SQ
Query Match 71.4%; Score 646; DB 19; Length 204;
Best Local Similarity 75.0%; Pred. No. 1.2e-60;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
QY 1 MFOIPEFSESEQEDSSAERGLGPGAGDGPSCGKHRRQAPGLLWDASHQEQPTSSSH 60
DB 43 mfiqpefepsegedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGGAGAVEITRSRHSYPAGTDEDEGMEEPSPPRGRSRAPPNLMWAQRYGRELRRMADE 120
DB 98 hggagameitrsrshssypagteedegmeelspfgrsrsappnlwaaqrygreilrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDNRNLGRGSSAPSQ 168
DB 158 fegsf-kglprpksagtatqmrqsagwttriqlgswdrnlkggtspsq 204
RESULT 10
ID AAB70369
XX AAB70369 standard; protein; 204 AA.
AC AAB70369;
XX 02-MAY-2001 (first entry)
XX Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
KW immunostimulant; neuroprotective; nootropic; antiischaemic; vulnerary;
KW cytostatic; antiviral; antiarthritic; antiinflammatory; wound healing;

KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
KW immunodeficiency disease; neurodegenerative disease; viral infection;
KW ischaemic cell death; reperfusion cell death; arthritis; infertility;
KW lymphoproliferative condition; inflammation; autoimmune disease.
XX Mus musculus.
OS Synthetic.
XX WO200110888-A1.
PN 15-FEB-2001.
PD 30-MAY-2000; 2000WO-US11864.
XX 28-MAY-1999; 99US-0136783.
PR (APOP-) APOPTOSIS TECHNOLOGY INC.
XX Zhou X;
PI WPI; 2001-138734/14.
XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
PT useful for screening for candidate compounds which induce or inhibit
PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
PT Ser113 -
XX Claim 4; Page 148; 157pp; English.
PS The present invention describes an isolated or synthetic polypeptide
XX (I) comprising a less than full length amino acid sequence of a mutant
CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
CC fragment, which contains amino acid substitutions at Ser118 of a human
CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
CC BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
CC nootropic, antiischaemic, vulnerary, cytostatic, antiviral,
CC antiarthritic, antiinflammatory and immunosuppressive activities, and
CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
CC polynucleotides can be used for screening candidate compounds and drugs
CC for activity that promote cell survival or apoptosis. Other uses include
CC inducing or inhibiting apoptosis in a cell. Candidate compounds
CC identified and (mutant) BAD polypeptides are useful in treating
CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
CC death, reperfusion cell death, wound healing, cancer, viral infections,
CC lymphoproliferative conditions, arthritis, infertility, inflammation and
CC autoimmune diseases. The present sequence represents a specifically
CC claimed longer murine BAD mutant amino acid sequence from the present
CC invention.
XX Sequence 204 AA;
SQ
Query Match 71.4%; Score 646; DB 22; Length 204;
Best Local Similarity 75.0%; Pred. No. 1.2e-60;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;
QY 1 MFOIPEFSESEQEDSSAERGLGPGAGDGPSCGKHRRQAPGLLWDASHQEQPTSSSH 60
DB 43 mfiqpefepsegedasatdrglgsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGGAGAVEITRSRHSYPAGTDEDEGMEEPSPPRGRSRAPPNLMWAQRYGRELRRMADE 120
DB 98 hggagameitrsrshssypagteedegmeelspfgrsrsappnlwaaqrygreilrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDNRNLGRGSSAPSQ 168
DB 158 fegsf-kglprpksagtatqmrqsagwttriqlgswdrnlkggtspsq 204
RESULT 11
ID AAW61317
XX AAW61317 standard; Protein; 204 AA.


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AC AAW61317;
XX 07-OCT-1998 (first entry)
XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX Mus sp.
XX Synthetic.
XX WO9817682-A1.
XX 30-APR-1998.
XX 17-OCT-1997; 97WO-US19175.
XX 18-OCT-1996; 96US-0733505.
XX (UNIW ) UNIV WASHINGTON.
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
XX N-PSDB; AAV27835.
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX
XX Claim 7; Page 60; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischaemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;

Query Match 71.0%; Score 643; DB 19; Length 204;
Best Local Similarity 74.4%; Pred. No. 2.5e-60;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHHQEQPTSSSH 60
DB 43 mfiqpefpepqedasadtrglgsitdqp---gpy--lapglglnhdgggraatnsh 97
QY 61 HGGAGAVIRSRSHSYPAGTDEDCMGEPSPFCRGRSRAPNLAOORYGRELRRMADE 120
DB 98 hggagameirsrshsyptagtedeemeelspfgrsraapnlaadrygrrelrmsde 157
QY 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
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DB 158 fegsf-kglprpksgatqmrsgagwtrilqsgwwdrnlkggstpsq 204
RESULT 12
AAW61316
ID AAW61316 standard; Protein; 204 AA.
XX
XX AAW61316;
XX
XX 07-OCT-1998 (first entry)
XX Mutant BCL-XL/BCL-2 associated cell death regulator #1.
XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
XX serine substituted mutant; apoptosis; cancer; viral infection.
XX
XX Mus sp.
XX Synthetic.
XX WO9817682-A1.
XX 30-APR-1998.
XX 17-OCT-1997; 97WO-US19175.
XX 18-OCT-1996; 96US-0733505.
XX (UNIW ) UNIV WASHINGTON.
XX Korsmeyer SJ;
XX
XX WPI; 1998-261422/23.
XX N-PSDB; AAV27834.
XX New mutant BAD polypeptide with phosphorylatable serine replaced -
XX useful for, e.g. treating reduced apoptosis such as in cancer or
XX viral infection
XX
XX Claim 7; Page 59; 95pp; English.
XX
XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX death regulator) proteins, having an amino acid other than Ser at
XX position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
XX present sequence represents a mutant BAD protein. Also described are: (1)
XX fragments of mutant BAD protein able to decrease cell viability; (2)
XX fusion proteins of mutant BAD with a heterologous polypeptide that
XX increases intracellular delivery. Mutant BAD proteins are used to treat
XX or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX viral infection, lymphoproliferation, arthritis, infertility,
XX inflammation and autoimmune disease. Polynucleotide sequences encoding
XX mutant BAD proteins can be used similarly by gene therapy or to produce
XX transgenic animals for use as disease models or in drug screening. BAD
XX proteins phosphorylated at specified Ser are used to screen for enhancers
XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX aging or ischaemic cell death. The apoptotic status of cells is
XX determined by measuring relative amounts of phosphorylated and non-
XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
XX greater death-promoting activity than wild-type BAD which can become
XX phosphorylated on the specified Ser, forming a product that does not
XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX proteins in the cytosol, thus promoting cell survival. The mutants with
XX Ser substituted cannot bind 14-3-3.
XX
XX Sequence 204 AA;

Query Match 70.7%; Score 640; DB 19; Length 204;
Best Local Similarity 73.8%; Pred. No. 5.2e-60;
Matches 124; Conservative 15; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPEFPESEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHHQEQPTSSSH 60
```

Db 43 mfiqifepseqedasatdrglqpsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMEEPSRGRSAPPNLWAAQRYGRELRRMADE 120
Db 98 hggagametrshsypagteedegmeelsprgrsraappnlwaaqrygreilrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
Db 158 fegsf-kgiprksagatqmrqsagwtrliqswdrnlgkggstpsq 204

RESULT 13
AAW61318
ID AAW61318 standard; Protein; 204 AA.
XX
AC AAW61318;
XX
DT 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #3.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO9817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1998-261422/23.
DR N-PSDB; AAV27836.
XX
PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
PS Claim 7; Page 60-61; 95pp; English.
XX
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX

SQ Sequence 204 AA;

Query Match 70.7%; Score 640; DB 19; Length 204;
Best Local Similarity 73.8%; Pred. No. 5.2e-60;
Matches 124; Conservative 15; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFOIPFEPSEQEDSSAERGLSGSPAGDQPSGSGKHROAPGLLWDASHOQBQPTSSSH 60
Db 43 mfiqifepseqedasatdrglqpsitedqp---gpy--lapglgslnhqggraatsnsh 97
QY 61 HGAGAVEIRSRHSSYPAGTDEDEGMEEPSRGRSAPPNLWAAQRYGRELRRMADE 120
Db 98 hggagametrshsypagteedegmeelsprgrsraappnlwaaqrygreilrmsde 157
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
Db 158 fegsf-kgiprksagatqmrqsagwtrliqswdrnlgkggstpsq 204

RESULT 14
AAW61319
ID AAW61319 standard; Protein; 59 AA.
XX
AC AAW61319;
XX
DT 07-OCT-1998 (first entry)
XX
DE Mutant BCL-XL/BCL-2 associated cell death regulator #4.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO9817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1998-261422/23.
DR N-PSDB; AAV27837.
XX
PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX
PS Claim 8; Page 73; 95pp; English.
XX
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is

CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.

Sequence	59 AA;
SQ	

Query Match 34.4%; Score 311; DB 19; Length 59;
Best Local Similarity 98.3%; Pred. NO. 7.7e-26;
Matches 58; Conservative 1; Mismatches 0; Indels

Qy	63	GAGAVEIRSRHSSYPACTEDDECMGEESPFRGRSRSAAPPNLWAAQYRGRELRMADDEF	121
Db	1	gagaveirsrhssypacteddecmgeespfrgrsrappnlwaaqyrrelrmsdef	59

RESULT 15

AAW61320
ID AAW61320 standard; protein; 59 AA.

AAW61320;

DT 07-OCT-1998 (first entry)

DE Mutant BCL-XL/BCL-2 associated cell death regulator #5.

Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein; serine substituted mutant; apoptosis; cancer; viral infection.

Mus sp.

OS Synthetic.

PN WO9817682-A1.

PD 30-APR-1998.

PF 17-OCT-1997; 97WO-US19175.

PR 18-OCT-1996; 96US-0733505.

PA (UNIW) UNIV WASHINGTON.

PI Korsmevcr SJ:

WPI: 1998-261422/23

DR N-PSDB; AAV27838.

PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection

PS Claim 8; Page 73; 95pp; English.

The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell death regulator) proteins, having an amino acid other than Ser at position 112 and/or 136, relative to the murine BAD 204 aa sequence. The present sequence represents a mutant BAD protein. Also described are: (1) fragments of mutant BAD protein able to decrease cell viability; (2) fusion proteins of mutant BAD with a heterologous polypeptide that increases intracellular delivery. Mutant BAD proteins are used to treat or prevent diseases associated with reduced apoptosis, e.g. cancer, viral infection, lymphoproliferation, arthritis, infertility, inflammation and autoimmune disease. Polynucleotide sequences encoding mutant BAD proteins can be used similarly by gene therapy or to produce transgenic animals for use as disease models or in drug screening. BAD proteins phosphorylated at specified Ser are used to screen for enhancers and inhibitors of serine-phosphatase. Inhibitors are potentially useful in treatment of excessive apoptosis such as AIDS, neurodegeneration, aging or ischaemic cell death. The apoptotic status of cells is

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:02:05 ; Search time 164.17 seconds
(without alignments)
227.023 Million cell updates/sec

Title: 09-580523-lb

Perfect score: 905

Sequence: 1 MFQIPEFPSEQEDSSAER.....RVFQSWDRNLGRGSSAPSQ 168

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCUS_COMB.pap.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pap.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pap.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pap.*
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- 10: /cgn2_6/ptodata/2/paa/US086_COMB.pap.*
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- 12: /cgn2_6/ptodata/2/paa/US088_COMB.pap.*
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- 20: /cgn2_6/ptodata/2/paa/US096_COMB.pap.*
- 21: /cgn2_6/ptodata/2/paa/US097_COMB.pap.*
- 22: /cgn2_6/ptodata/2/paa/US098_COMB.pap.*
- 23: /cgn2_6/ptodata/2/paa/US060_COMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	99.7	168	1	PCT-US00-11864-1
2	902	99.7	168	17	US-09-375-257-2
3	902	99.7	168	17	US-09-376-154-2
4	902	99.7	168	18	US-09-410-372-1
5	902	99.7	168	18	US-09-456-357-32
6	902	99.7	168	19	US-09-580-523-1
7	902	99.7	168	19	US-09-587-473-21
8	741	81.9	168	12	US-08-883-731-2
9	741	81.9	168	18	US-09-410-372-7
10	670	74.0	125	23	US-60-197-873-16338

11	646	71.4	162	1	PCT-US00-11864-3	Sequence 3, Appli
12	646	71.4	162	19	US-09-580-523-3	Sequence 3, Appli
13	646	71.4	204	1	PCT-US00-11864-2	Sequence 2, Appli
14	646	71.4	204	1	PCT-US97-15871-1	Sequence 1, Appli
15	646	71.4	204	1	PCT-US97-15871A-1	Sequence 1, Appli
16	646	71.4	204	1	PCT-US98-19765-41	Sequence 41, Appli
17	646	71.4	204	11	US-08-707-868-1	Sequence 1, Appli
18	646	71.4	204	11	US-08-733-505-1	Sequence 1, Appli
19	646	71.4	204	13	US-08-946-039-41	Sequence 41, Appli
20	646	71.4	204	19	US-09-580-523-2	Sequence 2, Appli
21	645	71.3	204	17	US-09-375-257-3	Sequence 3, Appli
22	645	71.3	204	17	US-09-376-154-3	Sequence 3, Appli
23	643	71.0	204	11	US-08-733-505-12	Sequence 12, Appli
24	643	71.0	204	11	US-08-733-505-13	Sequence 13, Appli
25	640	70.7	204	11	US-08-733-505-14	Sequence 14, Appli
26	640	70.7	587	20	US-09-639-245-4	Sequence 4, Appli
27	331	36.6	63	1	PCT-US97-15871A-12	Sequence 12, Appli
28	331	36.6	63	1	PCT-US98-19765-42	Sequence 42, Appli
29	331	36.6	63	13	US-08-946-039-42	Sequence 42, Appli
30	311	34.4	59	11	US-08-733-505-55	Sequence 55, Appli
31	308	34.0	59	11	US-08-733-505-56	Sequence 56, Appli
32	308	34.0	59	11	US-08-733-505-57	Sequence 57, Appli
33	305	33.7	59	11	US-08-733-505-58	Sequence 58, Appli
34	130	14.4	26	1	PCT-US00-11864-4	Sequence 4, Appli
35	130	14.4	26	1	PCT-US99-25285-5	Sequence 5, Appli
36	130	14.4	26	15	US-09-184-168A-5	Sequence 4, Appli
37	130	14.4	26	19	US-09-580-523-4	Sequence 4, Appli
38	129	14.3	25	20	US-09-656-399-10	Sequence 10, Appli
39	129	14.3	25	20	US-09-656-399A-10	Sequence 10, Appli
40	129	14.3	25	21	US-09-716-395-20	Sequence 20, Appli
41	126	13.9	25	20	US-09-656-399-17	Sequence 17, Appli
42	126	13.9	25	20	US-09-656-399A-17	Sequence 17, Appli
43	126	13.9	25	21	US-09-716-395-26	Sequence 26, Appli
44	125	13.8	25	20	US-09-656-399-15	Sequence 15, Appli
45	125	13.8	25	20	US-09-656-399-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
PCT-US00-11864-1
; Sequence 1, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-11864-1

Query Match	99.7%	Score	902;	DB	1;	Length	168;
Best Local Similarity	99.4%	Pred. No.	7.4e-71;				
Matches	167;	Conservative	1;	Mismatches	0;	Indels	0;
QY	1	MFQIPEPESQEDSSAERGLGSPAGDGGSGKHHRRQAPGLLWDASHOQEPTSSSH	60				
Db	1	MFQIPEPESQEDSSAERGLGSPAGDGGSGKHHRRQAPGLLWDASHOQEPTSSSH	60				
QY	61	HGGAGAVEIRSHSSYPAGTDEDDGMEEPSPFGRSRSPAPNLWAAOYRGELRRMADE	120				
Db	61	HGGAGAVEIRSHSSYPAGTDEDDGMEEPSPFGRSRSPAPNLWAAOYRGELRRMSDE	120				
QY	121	FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ	168				

Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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RESULT 2

US-09-375-257-2

; Sequence 2, Application US/09375257
; GENERAL INFORMATION:
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D1
; CURRENT APPLICATION NUMBER: US/09/375,257
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-375-257-2

Query Match 99.7%; Score 902; DB 17; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60
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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60
|||||

Qy 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMADE 120
|||||

Db 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMSDE 120
|||||

Qy 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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RESULT 3

US-09-376-154-2

; Sequence 2, Application US/09376154
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; TITLE OF INVENTION: ACIDS AND METHODS OF USE
; FILE REFERENCE: 480140.428D2
; CURRENT APPLICATION NUMBER: US/09/376,154
; CURRENT FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-376-154-2

Query Match 99.7%; Score 902; DB 17; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60
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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60
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Qy 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMADE 120
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Db 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMSDE 120
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Qy 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||

RESULT 4

US-09-410-372-1

; Sequence 1, Application US/09410372
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673

US-09-410-372-1

Query Match 99.7%; Score 902; DB 18; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60
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Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLDASHQOEPTSSSH 60
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Qy 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMADE 120
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Db 61 HGGAGAVEIRSRHSSYPACTDEDEGMGEPPSPFGRSRSAPPNLWAAQRYGRELRRMSDE 120
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Qy 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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RESULT 5

US-09-456-357-32

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; Sequence 32, Application US/09456357
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/09/456,357
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: 60/134,416
; EARLIER FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: 09/087,195
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/378,507
; EARLIER FILING DATE: 1995-01-26
; EARLIER APPLICATION NUMBER: 08/250,478
; EARLIER FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-357-32

Query Match          99.7%; Score 902; DB 18; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPSPFRGRSRAPPNLWAAQRYGRELRMADE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPSPFRGRSRAPPNLWAAQRYGRELRMSDE 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
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RESULT 6
US-09-580-523-1
; Sequence 1, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-523-1

Query Match          99.7%; Score 902; DB 19; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60
Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPSPFRGRSRAPPNLWAAQRYGRELRMADE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPSPFRGRSRAPPNLWAAQRYGRELRMSDE 120
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Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

RESULT 7
US-09-587-473-21
; Sequence 21, Application US/09587473
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Tsvetkov, Lyuben
; TITLE OF INVENTION: Protein Knockout Technology
; FILE REFERENCE: 44574-5047-WO
; CURRENT APPLICATION NUMBER: US/09/587,473
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/137,494
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-587-473-21

Query Match          99.7%; Score 902; DB 19; Length 168;
Best Local Similarity 99.4%; Pred. No. 7.4e-71;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60
Db 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60

Qy 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPSPFRGRSRAPPNLWAAQRYGRELRMADE 120
Db 61 HGGAGAVEIRSRHSSYPAGTDEDDGMEGEEPSPFRGRSRAPPNLWAAQRYGRELRMSDE 120

Qy 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWMDRNLGRGSSAPSQ 168

RESULT 8
US-08-883-731-2
; Sequence 2, Application US/08883731
; GENERAL INFORMATION:
; APPLICANT: Zhu, Li
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation Cell Death
; FILE REFERENCE: D6120
; CURRENT APPLICATION NUMBER: US/08/883,731
; CURRENT FILING DATE: 1997-06-27
; EARLIER APPLICATION NUMBER: US 08/665,617
; EARLIER FILING DATE: 1996-06-18
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; LOCATION:
; OTHER INFORMATION: Protein encoded by the BBC6 gene.
US-08-883-731-2

Query Match          81.9%; Score 741; DB 12; Length 168;
Best Local Similarity 84.5%; Pred. No. 9.3e-57;
Matches 142; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MFQIPEFSPQEDSSAERGLGSPAGDGPSSGKHHRRQAPGLLWDASHQOQPTSSSH 60
```

Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOEPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPACTEDDEGMGEPPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
Db 61 HGRWCGDPESPQLLPRDGGRRDGGGAQPFGRSRSAPPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 9
US-09-410-372-7
; Sequence 7, Application US/09410372
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-09-410-372-7

Query Match 81.9%; Score 741; DB 18; Length 168;
Best Local Similarity 84.5%; Pred. No. 9.3e-57;
Matches 142; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOEPTSSSH 60
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOEPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPACTEDDEGMGEPPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
Db 61 HGRWCGDPESPQLLPRDGGRRDGGGAQPFGRSRSAPPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

Db 121 FVDSFKKGLPRKSGAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
RESULT 10
US-60-197-873-16338
; Sequence 16338, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81 US1 PRO
; CURRENT APPLICATION NUMBER: US/60/197,873
; CURRENT FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 16338
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-197-873-16338

Query Match 74.0%; Score 670; DB 23; Length 125;
Best Local Similarity 99.2%; Pred. No. 1.1e-50;
Matches 124; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOEPTSSSH 60
Db 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOEPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPACTEDDEGMGEPPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120
Db 61 HGGAGAVEIRSRHSSYPACTEDDEGMGEPPSPFRGRSRSAPPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSF 125
Db 121 FVDSF 125

RESULT 11
PCT-US00-11864-3
; Sequence 3, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-3

Query Match 71.4%; Score 646; DB 1; Length 162;
Best Local Similarity 75.0%; Pred. No. 1.9e-48;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEFEPSEQEDSSAERGLGSPAGDPSGSGKHHRQAPGLLWDASHQOEPTSSSH 60
Db 1 MFQIPEFEPSEQEDASATDGLGSLTEDQP---GPY--LAPGLGSLNTHOOCRAATNSH 55
QY 61 HGGAGAVEIRSRHSSYPACTEDDEGMGEPPSPFRGRSRSAPPNLWAAQRYGRELRRMADE 120

D6 HGCGAGAMETRSHSSYPAGTEDEGMEELSPFRGRSRAPPNLWAAQRYGRELRMSDE 115

Gy FVDSFKGLPPRSAGTATQMROSSWTTRVFQSWDNRNLCRGSSAPSQ 168
| | ||||| | | | | : | | | | | | | | |

D6 FECSF-KGLPPRSAGTATMQSAGTRIQQSWDNRNLKGSTPSQ 162

```

RESULT 12
US-09-580-523-3
; Sequence 3, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-580-523-3

```

```

RESULT 13
PCT-US00-11864-2
; Sequence 2, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS,
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-2

```

Db	98	HGAGAMETRSHUSSYPAGTEDEGMEBELSPFRGRSRAPPNLWAAQRYGRELRRMSDE	157
Qy	121	FVDSFKGLPPRSAGTATOMROSSWTRVFQSWDRNLGRGSSPSQ	168
Db	158	FGESF-KGLPPRSAGTATOMROSSAGWTRIOSWDRNLKGCGSTPSO	204

RESULT 14
PCT-US97-15871-1
: Sequence 1, Application pc/TUS9715871
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, STANLEY J.
: TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
: TITLE OF INVENTION: PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH
: TITLE OF INVENTION: REGULATOR
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HOWELL & HAFERKAMP, L.C.
: STREET: 7733 FORSYTH BLVD., SUITE 1400
: CITY: ST. LOUIS
: STATE: MISSOURI
: COUNTRY: USA
: ZIP: 63146
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US97/15871
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: HOLLAND, DONALD R.
: REGISTRATION NUMBER: 35,197
: REFERENCE/DOCKET NUMBER: 965018
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (314) 727-5188
: TELEFAX: (314) 727-6092
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 204 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US97-15871-1

RESULT 15
PCT-US97-15871A-1
; Sequence 1, Application PC/TUS9715871A
; GENERAL INFORMATION:
; APPLICANT: KORMSEYER, STANLEY J
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE

Search completed: October 9, 2001, 16:02:05
Job time: 270 sec.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:04 ; Search time 28.81 seconds
(without alignments)
68.745 Million cell updates/sec

Title: US-09-580-523-1_COPY_143_168

Perfect score: 145

Sequence: 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26

Scoring table: BLOSUM62

Gapop 10.0 , -Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	82.8	204	2 A55671	bad protein - mous
2	57	39.3	3068	1 A44062	genome polyprotein
3	54	37.2	1632	2 C70752	probable ctpi prot
4	53	36.6	245	2 S68691	neutrophil granule
5	53	36.6	476	2 B83006	two-component resp
6	53	36.6	807	2 T39479	histone transcript
7	53	36.6	3163	1 JQ1895	genome polyprotein
8	51	35.2	855	2 F45557	external glycoprot
9	50.5	34.8	328	2 F75357	hypothetical prote
10	50	34.5	144	2 S29946	surface glycoprote
11	50	34.5	157	2 P00619	envelope protein -
12	50	34.5	243	2 B33329	cysteine-rich secr
13	50	34.5	264	2 T31521	hypothetical prote
14	50	34.5	299	2 B83081	hypothetical prote
15	50	34.5	634	2 A48335	cytoplasmic inclus
16	50	34.5	1170	1 TSHUPL	thrombospondin 1 p
17	50	34.5	1170	2 A40558	thrombospondin 1 p
18	50	34.5	3061	1 JN0545	genome polyprotein
19	50	34.5	3063	2 JS0166	genome polyprotein
20	49.5	34.1	335	2 T10074	cytochrome-c perox
21	49.5	34.1	358	1 Q1870	ALI protein - toma
22	49	33.8	226	2 S29952	surface glycoprote
23	49	33.8	242	2 P00626	envelope protein -
24	49	33.8	246	2 A24609	acidic epididymal
25	49	33.8	460	2 F84764	hypothetical prote
26	49	33.8	643	2 H83635	conserved hypothet
27	49	33.8	726	2 G83310	conserved hypothet
28	49	33.8	741	2 D83633	conserved hypothet
29	49	33.8	1148	2 T09073	splicing factor Si

30 49 33.8 1918 2 S43719
31 48 33.1 225 2 S29947
32 48 33.1 236 2 F85949
33 48 33.1 241 2 P00620
34 48 33.1 243 2 J80204
35 48 33.1 1501 2 C84512
36 48 33.1 3054 1 GNBVEV
37 47 32.4 170 2 A75513
38 47 32.4 426 2 T50944
39 47 32.4 462 1 S00552
40 47 32.4 691 2 F82987
41 47 32.4 1920 2 S43721
42 47 32.4 1926 2 S01169
43 46.5 32.1 110 2 D72701
44 46.5 32.1 202 2 T48709
45 46 31.7 119 2 T49363

ALIGNMENTS

RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999

C:Accession: A55671

R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A:Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361

A:Accession: A55671

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match 82.8%; Score 120; DB 2; Length 204;

Best Local Similarity 73.1%; Pred. No. 9.9e-10;

Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 QSSWTRVFQSWDRNLGRGSSAPSQ 26

||: |||: ||||| ||||: || |||

Db 179 QSAGWTRIIQSWDRNLGRGSGTPSQ 204

RESULT 2

A44062

genome polyprotein - pepper mottle virus (strain California)

N:Contains: 29K protein; 34K protein; coat protein; cylindrical inclusion protein; he

C:Species: pepper mottle virus

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001

C:Accession: A44062

R:Vance, V.B.; Moore, D.; Turpen, T.H.; Bracker, A.; Hollowell, V.C.

Virolgy 191, 19-30, 1992

A:Title: The complete nucleotide sequence of pepper mottle virus genomic RNA: compari

A:Reference number: A44062; MUID:93033110

A:Accession: A44062

A:Molecule type: genomic RNA

A:Residues: 1-3068 <VAN>

A:Cross-references: GB:M96425; NID:g332869; PIDN:AAA46903.1; PID:g332870

C:Superfamily: tobacco etch virus genome polyprotein

C:Keywords: ATP; coat protein; cylindrical inclusion protein; genome-linked protein;

F:1-287/Product: 34K protein #status predicted <KPT>

F:288-743/Product: helper component protein #status predicted <HCP>

F:744-1156/Product: 29K protein #status predicted <KPR>

F:1157-1790/Product: cylindrical inclusion protein #status predicted <CIP>

F:1241-1248/Region: nucleotide-binding motif A (P-loop)

F:1326-1331/Region: nucleotide-binding motif B

F:1330-1333/Region: DEXH motif

F:1791-2276/Product: nuclear inclusion protein a #status predicted <NIA>

F;2277-2799/Product: nuclear inclusion protein b #status predicted <NTB>
 F;2800-3068/Product: coat protein #status predicted <CPT>
 F;1906/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 39.3%; Score 57; DB 1; Length 3068;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 FOSWDRNLGRSSAP 24
 I:|||||:|||||
 Db 1191 FESWDEQVARGFTIP 1206

RESULT 3
 C70752
 Probable ctpI protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: C70752
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: C70752
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1632 <COL>
 A:Cross-references: GB:Z74410; GB:AL123456; PIDN:CAA98940.1; PID:el299890;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: ctpI
 C:Superfamily: ATPase nucleotide-binding domain homology
 F;1237-1406/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 37.2%; Score 54; DB 2; Length 1632;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 13 WDRNLGRSSAPSQ 26
 |||||
 Db 1576 WDRSPGRASSAPRQ 1589

RESULT 4
 S68691
 neutrophil granules matrix glycoprotein SGP28 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
 C:Accession: S68691; S74313; S68683
 R;Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.
 FEBS Lett. 380, 246-250, 1996
 A:Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophils with a novel domain
 A:Reference number: S68691; MUID:96186934
 A:Accession: S68691
 A:Molecule type: mRNA
 A:Residues: 1-245 <KJE>
 A:Cross-references: EMBL:X94333; NID:gl213612; PIDN:CAA63984.1; PID:gl213613
 A:Accession: S74313
 A:Molecule type: protein
 A:Residues: 33-83;96-143;165-217;221-226 <KJL>
 R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuniger, J.
 Eur. J. Biochem. 236, 827-836, 1996
 A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and function
 A:Reference number: S68681; MUID:96270732
 A:Accession: S68683
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-105;107-245 <KRA>

A:Cross-references: EMBL:X95240; NID:gl262818; PIDN:CAA64527.1; PID:gl262819
 C:Genetics:
 A:Gene: SGP28
 C:Superfamily: cysteine-rich secretory protein 1
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <MA

Query Match 36.6%; Score 53; DB 2; Length 245;
 Best Local Similarity 37.0%; Pred. No. 3.3;
 Matches 10; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 3 SSWTRVFQSWDR----NLGRSSAPS 25
 |||||:|||||
 Db 107 SWSQAIQSWFDEYNDFGCGPKTPN 133

RESULT 5
 E83006
 two-component response regulator NtrC PA5125 [imported] - Pseudomonas aeruginosa (str
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: E83006
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
 A:Reference number: A82950; MUID:20437337
 A:Accession: E83006
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-476 <STO>
 A:Cross-references: GB:AE004925; GB:AE004091; NID:g9951415; PIDN:AA08510.1; GSPDB:GN
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: ntrC; PA5125
 C:Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo

Query Match 36.6%; Score 53; DB 2; Length 476;
 Best Local Similarity 38.1%; Pred. No. 6.4;
 Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNLGRSS 22
 ::|||:|:|||||
 Db 396 AANWEQALRWADQALGRGQS 416

RESULT 6
 T39479
 histone transcription regulator beta-transducin homolog - fission yeast (Schizosaccha
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000
 C:Accession: T39479
 R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21858
 A:Accession: T39479
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-807 <LYN>
 A:Cross-references: EMBL:AL031349; PIDN:CAA20478.1; GSPDB:GN00067; SPDB:SPBC15D4.03
 A:Experimental source: strain 972h-; cosmid cl5D4
 C:Genetics:
 A:Gene: SPDB:SPBC15D4.03
 A:Map position: 2
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 36.6%; Score 53; DB 2; Length 807;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWW 13
||||| : :
Db 624 SSSWLRVSGW 635

RESULT 7

genome polyprotein - turnip mosaic virus
N:Contains: coat protein; cytoplasmic inclusion protein; helper component protein; nucleocapsid protein
C:Species: turnip mosaic virus, TuMV
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
C:Accession: JQ1895; JQ1168; JQ0217
R:Nicolas, O.; Laliberte, J.F.
J. Gen. Virol. 73, 2785-2793, 1992
A:Title: The complete nucleotide sequence of turnip mosaic polyvirus RNA.
A:Reference number: JQ1895; MUID:93057350
A:Accession: JQ1895
A:Molecule type: mRNA
A:Residues: 1-3163 <NIC>
A:Cross-references: DBJ:D10927; NID:g222660; PIDN:BAA01725.1; PID:g222661
A:Experimental source: strain Quebec
R:Tremblay, M.F.; Nicolas, O.; Sinha, R.C.; Lazure, C.; Laliberte, J.F.
J. Gen. Virol. 71, 2769-2772, 1990
A:Title: Sequence of the 3'-terminal region of turnip mosaic virus RNA and the capsid protein
A:Reference number: JQ1168; MUID:91073142
A:Accession: JQ1168
A:Molecule type: genomic RNA
A:Residues: 1534-2861, G, 2863-3163 <TRE>
A:Cross-references: GB:D10601; GB:D01090; NID:g222658; PIDN:BAA01452.1; PID:g222659
A:Accession: PQ0217

A:Molecule type: protein
A:Residues: 2876-2892; 2929-2941; 3118-3141 <TR2>
C:Superfamily: tobacco etch virus genome polyprotein
C:Keywords: ATP; coat protein; genome-linked protein; inclusion protein; nucleotide binding site
F:1-362/Product: P1 protein #status predicted <PIP>
F:363-820/Product: helper component protein #status predicted <HCP>
F:821-1175/Product: P3 protein #status predicted <P3p>
F:1176-1227/Product: p6K1 protein #status predicted <P6p>
F:1228-1870/Product: cytoplasmic inclusion protein #status predicted <CIP>
F:1313-1320/Region: nucleotide-binding motif A (P-loop)
F:1398-1403/Region: nucleotide-binding motif B
F:1402-1405/Region: DEHX motif
F:1871-1923/Product: p6K2 protein #status predicted <PKP>
F:1924-2115/Product: VPg protein #status predicted <VPG>
F:2116-2358/Product: nuclear inclusion A protein #status predicted <NIA>
F:2359-2875/Product: nuclear inclusion B protein #status predicted <NIB>
F:2876-3163/Product: coat (capsid) protein #status experimental <CAP>
F:1986/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 36.6%; Score 53; DB 1; Length 3163;
Best Local Similarity 44.4%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 7 RVFQSWDRNLGRGSSAP 24
: ||||| : : :
Db 1261 KTFASWWSHQLSRGTIP 1278

RESULT 8

external glycoprotein; transmembrane protein (external glycoprotein, EGP, transmembrane protein)
C:Species: feline immunodeficiency virus
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C:Accession: F45557
R:Maki, N.; Miyazawa, T.; Fukasawa, M.; Hasegawa, A.; Hayami, M.; Miki, K.; Mikami, T.
Arch. Virol. 123, 29-45, 1992
A:Title: Molecular characterization and heterogeneity of feline immunodeficiency virus isolates
A:Reference number: A45557; MUID:92198230
A:Accession: F45557
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-855 <MAK>
A:Experimental source: strain TM2
A:Note: sequence extracted from NCBI backbone (NCBI:89826, NCBIP:89854)
C:Superfamily: feline immunodeficiency virus env polyprotein
C:Keywords: glycoprotein; transmembrane protein

Query Match 35.2%; Score 51; DB 2; Length 855;
Best Local Similarity 56.2%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWMDRN 16
||| : : :
Db 383 QSGSWIRTISSWKQRN 398

RESULT 9

F75357
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75357
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75357
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <WHI>
A:Cross-references: GB:AE002017; GB:AE000513; NID:g6459527; PIDN:AAF11318.1; PID:g6459527
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1757
A:Map position: 1

Query Match 34.8%; Score 50.5; DB 2; Length 328;
Best Local Similarity 41.7%; Pred. No. 9.9;
Matches 10; Conservative 3; Mismatches 6; Indels 5; Gaps 2;

QY 1 QSSWTRVFQSWDRNLGRGSSAP 24
: ||||| : : :
Db 83 EHGWTNR----WWNRQ-GRGMPSP 101

RESULT 10

S29946
surface glycoprotein - feline immunodeficiency virus (fragment)
C:Species: feline immunodeficiency virus
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S29946
R:Rigby, M.A.
submitted to the EMBL Data Library, November 1992
A:Reference number: S29946
A:Accession: S29946
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-144 <RIG>
A:Cross-references: EMBL:X69495; NID:g59269; PIDN:CAA49249.1; PID:g938167
C:Superfamily: feline immunodeficiency virus env polyprotein
C:Keywords: glycoprotein

Query Match 34.5%; Score 50; DB 2; Length 144;
Best Local Similarity 56.2%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWMDRN 16
: ||||| : : :
Db 1261 KTFASWWSHQLSRGTIP 1278

Db 41 QPGSWLRVSSWKORN 56

RESULT 11

PQ0619

envelope protein - feline immunodeficiency virus (isolate UK 5) (fragment)

C:Species: feline immunodeficiency virus

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999

C:Accession: PQ0619

R:Rigby, M.A.; Holmes, E.C.; Pistello, M.; Mackay, A.; Brown, A.J.L.; Neill, J.C.

J. Gen. Virol. 74, 425-436, 1993

A:Title: Evolution of structural proteins of feline immunodeficiency virus: Molecular evolution

A:Reference number: JQ2003; MUID:93187604

A:Accession: PQ0619

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-157 <RIG>

A:Cross-references: GB:X69495

C:Genetics:

A:Gene: env

C:Superfamily: feline immunodeficiency virus env polyprotein

C:Keywords: envelope protein; glycoprotein

F:92/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.5%; Score 50; DB 2; Length 157;

Best Local Similarity 56.2%; Pred. No. 5.5;

Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWDRN 16

Db 57 QPGSWLRVSSWKORN 72

RESULT 12

B33329

cysteine-rich secretory protein 2 type I precursor - human

N:Alternate names: testis-specific protein

C:Species: Homo sapiens (man)

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Jun-2000

C:Accession: B33329; S68682

R:Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.

Genomics 5, 527-534, 1989

A:Title: Cloning and mapping of a testis-specific gene with sequence similarity to a sperm

A:Reference number: A33329; MUID:90129048

A:Accession: B33329

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-243 <RAS>

A:Cross-references: GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883

R:Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuniger, J. J. Biochem. 236, 837-836, 1996

A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and

A:Reference number: S68681; MUID:96270732

A:Accession: S68682

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-243 <KRA>

A:Cross-references: EMBL:X95239; NID:g1262816; PIDN:CAA64526.1; PID:g1262817

C:Genetics:

A:Gene: GDB:TPX1

A:Cross-references: GDB:I20760; OMIM:187430

A:Map position: 6p21-6qter

C:Superfamily: cysteine-rich secretory protein 1

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-243/Product: cysteine-rich secretory protein 2 type I #status predicted <MAT>

Query Match 34.5%; Score 50; DB 2; Length 243;

Best Local Similarity 37.0%; Pred. No. 8.6;

Matches 10; Conservative 5; Mismatches 8; Indels 4; Gaps 1;

QY 3 SSWTRVFQSWDRNL-----GRGSAPS 25

Db 105 TSWSSAIQSWYDEILDVYGVGPKSPN 131

RESULT 13

T31521

hypothetical protein Y116A8C.23 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000

C:Accession: T31521

R:McMurray, A.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21041

A:Accession: T31521

A:Status: preliminary; translated from GB/EMBL/DDBU

A:Molecule type: DNA

A:Residues: 1-264 <WIL>

A:Cross-references: EMBL:AL117204; PIDN:CAB55155.1; CESP:Y116A8C.23

A:Experimental source: clone Y116A8C

C:Genetics:

A:Gene: CESP:Y116A8C.23

A:Introns: 42/3; 102/3; 178/3; 213/3

C:Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.23

Query Match 34.5%; Score 50; DB 2; Length 264;

Best Local Similarity 56.2%; Pred. No. 9.3;

Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 11 SMDWNLGRGSSAPSQ 26

Db 235 SYWERTGRARSASQ 250

RESULT 14

B83081

hypothetical protein PA4512 [imported] - Pseudomonas aeruginosa (strain PAO1)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83081

R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adaman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: B83081

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-299 <STO>

A:Cross-references: GB:AE004865; GB:AE004091; NID:g9950752; PIDN:AAG07900.1; GSPDB:GN

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA4512

Query Match 34.5%; Score 50; DB 2; Length 299;

Best Local Similarity 29.2%; Pred. No. 11;

Matches 7; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 2 SSSWTRVFQSWDRNLGRGSSAPS 25

Db 224 TQGWATAFNRWFSRNVMAAAPN 247

RESULT 15

A48335

cytoplasmic inclusion protein - potato virus Y (strain O)

C:Species: potato virus Y, PVY

C>Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 02-Feb-2001

C:Accession: A48335

R:Ohshima, K.; Inoue, A.K.; Shikata, E.

Arch. Virol. 128, 15-27, 1993

A:Title: Molecular cloning, sequencing, and expression in Escherichia coli of the potato
A:Reference number: A48335; MUID:93119268
A:Accession: A48335
A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-634 <OHS>
A:Cross-references: GB:S51663; NID:g262852; PIDN:AAB24777.1; PID:g262853
A>Note: sequence extracted from NCBI backbone (NCBIN:121707, NCBIP:121709)
C:Superfamily: tobacco etch virus genome polyprotein
C:Keywords: nucleotide binding; P-loop
F:85-92/Region: nucleotide-binding motif A (P-loop)

Query Match 34.5%; Score 50; DB 2; Length 634;
Best Local Similarity 43.8%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 9 FQSWWDRNLGRGSSAP 24
| | | | | : | : |
Db 35 FSDWWDRQIQMGHTLP 50

Search completed: October 9, 2001, 15:54:05
Job time: 235 sec

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; Entered [jdelaval 9-Oct-01 15:43]
09-580523-1A
MFOIPEPEPSEQEDSSSAERGLGPGSPAGDGPSCGKHHRQAPGLLWDASHQOEQPTSSSHHGGAGAVEIR
SRHSSYPAGTDEDEGMGEPSPPFRGRSRSAFNNLWAAQRYGRELRRMDEFDSEFKKGLPRPKSAGTATQ
MRQSSSWTRVTFQSWWDRNLGRGSSAPSQ1

Part 2

; Entered [jdelaval 9-Oct-01 15:46]
09-580523-1B
MFOIPEPEPSEQEDSSSAERGLGPGSPAGDGPSCGKHHRQAPGLLWDASHQOEQPTSSSHHGGAGAVEIR
SRHSSYPAGTDEDEGMGEPSPPFRGRSRSAFNNLWAAQRYGRELRRMDEFDSEFKKGLPRPKSAGTATQ
MRQSSSWTRVTFQSWWDRNLGRGSSAPSQ1

Part 3

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	112	100.0	166	1	US-08-665-617-2		Sequence 2, Appli
2	112	100.0	168	2	US-08-717-133-2		Sequence 2, Appli
3	112	100.0	168	3	US-08-985-335-1		Sequence 1, Appli
4	112	100.0	168	3	US-08-985-335-7		Sequence 7, Appli
5	102	91.1	23	1	US-08-333-565-10		Sequence 10, Appli
6	102	91.1	23	2	US-08-661-479-10		Sequence 10, Appli
7	102	91.1	23	2	US-08-733-505A-55		Sequence 10, Appli
8	102	91.1	59	2	US-08-733-505A-56		Sequence 55, Appli
9	102	91.1	59	2	US-08-733-505A-57		Sequence 56, Appli
10	102	91.1	59	2	US-08-733-505A-58		Sequence 57, Appli
11	102	91.1	204	1	US-08-333-565-2		Sequence 58, Appli
12	102	91.1	204	2	US-08-333-565-2		Sequence 2, Appli
13	102	91.1	204	2	US-08-733-505A-1		Sequence 1, Appli
14	102	91.1	204	2	US-08-733-505A-12		Sequence 12, Appli
15	102	91.1	204	2	US-08-733-505A-13		Sequence 13, Appli
16	102	91.1	204	2	US-08-733-505A-14		Sequence 14, Appli
17	99	88.4	204	2	US-08-717-123-3		Sequence 3, Appli
18	86	76.8	16	1	US-08-333-565-26		Sequence 26, Appli
19	86	76.8	16	2	US-08-661-479-26		Sequence 26, Appli
20	61	54.5	11	2	US-08-733-505A-34		Sequence 34, Appli
21	61	54.5	11	2	US-08-706-741B-69		Sequence 69, Appli
22	61	54.5	11	2	US-08-924-695A-69		Sequence 69, Appli
23	45	40.2	380	1	US-08-153-848-40		Sequence 40, Appli
24	45	40.2	380	3	US-08-153-848-40		Sequence 40, Appli
25	45	40.2	380	5	US-09-299-843A-40		Sequence 40, Appli
26	44	39.3	587	4	US-09-147-923-2		Sequence 2, Appli
27	44	39.3	1008	2	US-08-680-336-30		Sequence 30, Appli

RESULT 2
US-08-717-123-2
; Sequence 1, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match 100.0%; Score 112; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 103 NLWAAQRYGRELRRMSDEFVD 123
RESULT 3
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1

Query Match 100.0%; Score 112; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 103 NLWAAQRYGRELRRMSDEFVD 123

RESULT 4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-08-985-335-7

Query Match 100.0%; Score 112; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
|||||
DB 103 NLWAAQRYGRELRRMSDEFVD 123

RESULT 5
US-08-333-565-10
; Sequence 10, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2422
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 91.1%; Score 102; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||
DB 3 NLWAAQRYGRELRRMSDEF 21

RESULT 6
US-08-661-479-10
; Sequence 10, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-10

Query Match 91.1%; Score 102; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||
DB 3 NLWAAQRYGRELRRMSDEF 21

RESULT 7
US-08-733-505A-55
; Sequence 55, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-55

Query Match 91.1%; Score 102; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 8.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||

Db 41 NLWAAQRYGRELRRMSDEF 59

RESULT 8
US-08-733-505A-56
Sequence 56, Application US/087333505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-56

Query Match 91.1%; Score 102; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 8.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||

Db 41 NLWAAQRYGRELRRMSDEF 59

RESULT 9
US-08-733-505A-57
Sequence 57, Application US/087333505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-57

Query Match 91.1%; Score 102; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 8.2e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||

Db 41 NLWAAQRYGRELRRMSDEF 59

RESULT 10
US-08-733-505A-58
Sequence 58, Application US/087333505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-58

Query Match 91.1%; Score 102; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 8.2e-10; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NLWAAQRYGRELRRMSDEF 19
Db 41 NLWAAQRYGRELRRMSDEF 59
RESULT 11
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."
US-08-333-565-2

Query Match 91.1%; Score 102; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 3e-09; Mismatches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NLWAAQRYGRELRRMSDEF 19
Db 140 NLWAAQRYGRELRRMSDEF 158
RESULT 12
US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."
US-08-661-479-2

RESULT 14
US-08-733-505A-12
; Sequence 12, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS
LENGTH: 204 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 91.1%; Score 102; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEF 19
| | | | | | | | | | | | | | | | | | | | | |
Db 140 NLWAAQRYGRELRRMSDEF 158

Search completed: October 9, 2001, 15:52:36
Job time: 151 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:08:31 ; Search time 36.31 Seconds
(without alignments)
27.430 Million cell updates/sec

Title: US-09-580-523-1_COPY_103_123
Perfect score: 112
Sequence: 1 NLWAAQRYGRELRLMSDEFVD 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 311045 seqs, 47428042 residues

Total number of hits satisfying chosen parameters: 311045

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New.*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	125	5	US-09-834-366-16338
2	112	100.0	168	5	US-09-922-378-2
3	112	100.0	201	1	PCT-US01-18569-2762
4	99	88.4	204	5	US-09-922-378-3
5	50	44.6	232	5	US-09-902-540-9711
6	46	41.1	483	1	PCT-US01-08631-38983
7	46	41.1	484	5	US-09-902-540-13700
8	45	40.2	380	5	US-09-088-337B-40
9	43.5	38.8	168	1	PCT-US01-08631-43907
10	43.5	38.8	681	1	PCT-US01-08631-52397
11	43	38.4	100	5	US-09-758-475-257
12	43	38.4	270	1	PCT-US01-26189-162
13	43	38.4	270	5	US-09-934-455-162
14	42.5	37.9	572	5	US-09-902-540-13770
15	42	37.5	262	5	US-09-803-110-9772
16	42	37.5	526	5	US-09-573-655A-1977
17	41.5	37.1	189	5	US-09-803-110-11897
18	41.5	37.1	465	1	PCT-US01-08631-35041
19	41	36.6	83	5	US-09-834-366-26246
20	41	36.6	208	1	PCT-US01-08631-37956
21	41	36.6	208	1	PCT-US01-08631-41486
22	41	36.6	209	1	PCT-US01-08631-44176
23	41	36.6	292	5	US-09-738-626-4426
24	41	36.6	319	5	US-09-927-796-64
25	41	36.6	362	5	US-09-925-298-617
26	41	36.6	848	5	US-09-902-540-10014
27	40.5	36.2	380	1	PCT-US01-08631-37140

28 40.5 36.2 877 1 PCT-US01-14827-15394 Sequence 15394, A
29 40.5 36.2 1309 1 PCT-US01-14827-15396 Sequence 15396, A
30 40.5 36.2 1350 1 PCT-US01-14827-15390 Sequence 15390, A
31 40 35.7 69 5 US-09-649-866A-2290 Sequence 2290, Ap
32 40 35.7 126 5 US-09-875-195-746 Sequence 746, App
33 40 35.7 126 5 US-09-758-453-337 Sequence 337, App
34 40 35.7 141 1 PCT-US01-08631-51026 Sequence 51026, A
35 40 35.7 172 5 US-09-758-466-567 Sequence 567, App
36 40 35.7 243 5 US-09-803-110-10646 Sequence 10646, A
37 40 35.7 294 5 US-09-803-110-11563 Sequence 11563, A
38 40 35.7 398 1 PCT-US01-08631-38702 Sequence 38702, A
39 40 35.7 447 1 PCT-US01-08631-48287 Sequence 48287, A
40 40 35.7 463 1 PCT-US01-08631-53631 Sequence 53631, A
41 40 35.7 568 5 US-09-902-540-14309 Sequence 14309, A
42 40 35.7 663 6 US-60-312-544-10009 Sequence 10009, A
43 40 35.7 1241 1 PCT-US01-08631-36270 Sequence 36270, A
44 39.5 35.3 112 5 US-09-595-332A-1432 Sequence 1432, Ap
45 39 34.8 83 5 US-09-834-366-18666 Sequence 18666, A

ALIGNMENTS

RESULT 1
US-09-834-366-16338
; Sequence 16338, Application US/09834366
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: 81. US2. REG
; CURRENT APPLICATION NUMBER: US/09/834, 366
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197, 873
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 52153
; SOFTWARE: Patent.pm
; SEQ ID NO 16338
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-366-16338

Query Match 100.0%; Score 112; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLWAAQRYGRELRLMSDEFVD 21
Db 103 NLWAAQRYGRELRLMSDEFVD 123

RESULT 2
US-09-922-378-2
; Sequence 2, Application US/09922378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Ollersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922, 378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-922-378-2

Query Match 100.0%; Score 112; DB 5; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
|||||

Db 103 NLWAAQRYGRELRRMSDEFVD 123

RESULT 3

PCT-US01-18569-2762
; Sequence 2762, Application PC/TUS0118569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA133PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2762
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (146)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (169)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-2762

Query Match 100.0%; Score 112; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
|||||

Db 111 NLWAAQRYGRELRRMSDEFVD 131

RESULT 4

US-09-922-378-3
; Sequence 3, Application US/09922378
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: HUMAN BAD POLYPEPTIDES, ENCODING NUCLEIC
; FILE REFERENCE: 480140.428D3
; CURRENT APPLICATION NUMBER: US/09/922,378
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-922-378-3

Query Match 88.4%; Score 99; DB 5; Length 204;
Best Local Similarity 94.7%; Pred. No. 4e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||

Db 140 NLWAAQRYGRELRRMTDEF 158

RESULT 5

US-09-902-540-9711
; Sequence 9711, Application US/09902540
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9711
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9711

Query Match 44.6%; Score 50; DB 5; Length 232;
Best Local Similarity 50.0%; Pred. No. 2.2;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDE 18
|||

Db 157 SLWIGHRWGKGLRRMHCE 174

RESULT 6

PCT-US01-08631-38983
; Sequence 38983, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 38983
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (41)..(93)
; OTHER INFORMATION: Heat shock hsp70 proteins family proteins domain identified
; OTHER INFORMATION: by eMATRIX, accession number BL00297C, p-value=1.000e-40, raw
; OTHER INFORMATION: of 9.51
; NAME/KEY: DOMAIN
; LOCATION: (1)..(450)
; OTHER INFORMATION: Hsp70 protein domain identified by Pfam, accession name
; OTHER INFORMATION: HSP70, E-value=3.2e-153, Pfam score of 522.4
; NAME/KEY: misc_feature
; LOCATION: (1)...(483)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2

PCT-US01-08631-38983

Query Match 41.1%; Score 46; DB 1; Length 483;
Best Local Similarity 38.9%; Pred. No. 21;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDE 18
|:|:|:|:|:|:|:|:|:|:|:
Db 355 NIWSAEKYKAEDKQRDK 372

RESULT 7

US-09-902-540-13700
; Sequence 13700, Application US/09902540

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 13700

; LENGTH: 484

; TYPE: PRT

; ORGANISM: Myxococcus xanthus

US-09-902-540-13700

Query Match 41.1%; Score 46; DB 5; Length 484;
Best Local Similarity 72.7%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WAAQRYGREL 13
|:|:|:|:|:|:|:|:|:|:|:
Db 342 WAAVHGRELK 352

RESULT 8

US-09-088-337B-40

; Sequence 40, Application US/09088337B

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: Novel Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/088,337B

; FILING DATE: 01-Jun-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/153,848

; FILING DATE: 17-NOV-1993

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Noland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 40:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 380 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-088-337B-40

Query Match 40.2%; Score 45; DB 5; Length 380;
Best Local Similarity 47.4%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LWAAQRYGRELRRMSDEFV 20
|:|:|:|:|:|:|:|:|:|:|:
Db 50 LWTVFRSSREKRRSADIFI 68

RESULT 9

PCT-US01-08631-43907

; Sequence 43907, Application PC/TUS0108631

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-049

; CURRENT APPLICATION NUMBER: PCT/US01/08631

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 43907

; LENGTH: 168

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US01-08631-43907

Query Match 38.8%; Score 43.5; DB 1; Length 168;
Best Local Similarity 38.1%; Pred. No. 17;
Matches 8; Conservative 7; Mismatches 3; Indels 3; Gaps 1;

Qy 1 NLWAAQRYGRELRRMSDEFV 21
|:|:|:|:|:|:|:|:|:|:|:
Db 106 DWCC--HGKKIRRPAGEFVD 123

RESULT 10

PCT-US01-08631-52397

; Sequence 52397, Application PC/TUS0108631

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-049

; CURRENT APPLICATION NUMBER: PCT/US01/08631

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

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; SOFTWARE: Custom
; SEQ ID NO 52397
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(33)
; OTHER INFORMATION: ALPHA-2A ADRENERGIC RECEPTOR SIGNATURE domain identified by
; OTHER INFORMATION: eMATRIX, accession number PR00558C, p-value=7.330e-09, raw score
; OTHER INFORMATION: 6.54
; NAME/KEY: DOMAIN
; LOCATION: (421)..(509)
; OTHER INFORMATION: PCI domain identified by Pfam, accession name PCI, E-value=
; OTHER INFORMATION: 2.1e-13, Pfam score of 58.0
; NAME/KEY: misc_feature
; LOCATION: (1)..(681)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-52397
```

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Query Match 38.8%; Score 43.5; DB 1; Length 681;
Best Local Similarity 55.6%; Pred. No. 76;
Matches 10; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 3 WAAQRYGRELRRMSD-EF 19
   : || || | | | |
Db 525 WSLQNRGRERRNKQDLEF 542
```

```
RESULT 11
US-09-758-475-257
; Sequence 257, Application US/09758475
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM035
; CURRENT APPLICATION NUMBER: US/09/758,475
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-475-257
```

```
Query Match 38.4%; Score 43; DB 5; Length 100;
Best Local Similarity 45.0%; Pred. No. 11;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFV 20
   : || | | | |
Db 20 NMWAAQLTGKGRRWQVFEV 39
```

```
RESULT 12
PCT-US01-26189-162
; Sequence 162, Application PC/TUS0126189
; GENERAL INFORMATION:
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
```

```
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Adam, Luc
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0024
; CURRENT APPLICATION NUMBER: PCT/US01/26189
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 464
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
PCT-US01-26189-162
```

```
Query Match 38.4%; Score 43; DB 1; Length 270;
Best Local Similarity 40.0%; Pred. No. 33;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFV 20
   : || | | | |
Db 78 NMEQPIYGRDFKRSSSMV 97
```

```
RESULT 13
US-09-934-455-162
; Sequence 162, Application US/09934455
; GENERAL INFORMATION:
; APPLICANT: Adam, Luc
; APPLICANT: Creelman, Robert
; APPLICANT: Dubell, Arnold
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Keddle, James
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pineda, Omaira
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV
; FILE REFERENCE: MBI-0025
; CURRENT APPLICATION NUMBER: US/09/934,455
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227439
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: MBI-0022
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: MBI-0023
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 516
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-934-455-162
```

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Query Match 38.4%; Score 43; DB 5; Length 270;
Best Local Similarity 40.0%; Pred. No. 33;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:53:27 ; Search time 44.37 seconds
(without alignments)
28.693 Million cell updates/sec

Title: US-09-580-523-1_copy_103_123

Perfect score: 112

Sequence: 1 NLWAAQRYGRELRLRMSDFVD 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	166	18	AAW32476
2	112	100.0	168	19	AAW55779
3	112	100.0	168	21	AAW33512
4	112	100.0	168	22	AAW70368
5	112	100.0	168	22	AAW48287
6	102	91.1	23	17	AAW95166
7	102	91.1	26	21	AAW37001
8	102	91.1	26	21	AAW37002
9	102	91.1	27	21	AAW37003
10	102	91.1	27	21	AAW37056
11	102	91.1	28	21	AAW37055

12	102	91.1	59	19	AAW61319	Mutant BCL-XL/BCL-
13	102	91.1	59	19	AAW61320	Mutant BCL-XL/BCL-
14	102	91.1	59	19	AAW61321	Mutant BCL-XL/BCL-
15	102	91.1	59	19	AAW61322	Mutant BCL-XL/BCL-
16	102	91.1	162	22	AAW70370	Shorter murine BAD
17	102	91.1	204	17	AAW95168	bcl-x(L)/bcl-2 ass
18	102	91.1	204	19	AAW61315	Murine BCL-XL/BCL-
19	102	91.1	204	19	AAW61316	Mutant BCL-XL/BCL-
20	102	91.1	204	19	AAW61317	Mutant BCL-XL/BCL-
21	102	91.1	204	19	AAW61318	Mutant BCL-XL/BCL-
22	102	91.1	204	19	AAW58832	Murine BAD protein
23	102	91.1	204	22	AAW70369	Longer murine BAD
24	91	81.2	26	21	AAW96321	Mammalian Bad Bcl-
25	91	81.2	26	22	AAW70371	BAD BH3 consensus
26	86	76.8	16	17	AAW95163	bcl-x(L)/bcl-2 ass
27	83	74.1	16	20	AAW05421	Human BAD BH3 doma
28	83	74.1	16	21	AAW37029	Bcl2 polypeptide B
29	75	67.0	18	22	AAW70379	BAD BH3 domain reg
30	75	67.0	20	22	AAW70380	BAD BH3 domain reg
31	73	65.2	16	20	AAW05422	Mouse BAD BH3 doma
32	73	65.2	16	21	AAW37028	Bcl2 polypeptide B
33	46	41.1	16	21	AAW37046	Bcl2 polypeptide B
34	46	41.1	26	21	AAW97352	Mammalian Bim Bcl-
35	46	41.1	26	22	AAW70378	BIM BH3 consensus
36	46	41.1	27	21	AAW37019	Bcl2 polypeptide B
37	46	41.1	138	20	AAW98164	Human Bim-L mutant
38	46	41.1	138	20	AAW98165	Human Bim-L mutant
39	46	41.1	138	20	AAW98166	Human Bim-L mutant
40	46	41.1	138	20	AAW98167	Human Bim-L mutant
41	46	41.1	138	20	AAW98168	Human Bim-L mutant
42	46	41.1	138	20	AAW98157	Human Bim-L mutant
43	46	41.1	198	20	AAW98158	Human Bcl-2 intera
44	45	40.2	377	22	AAW48502	Mouse APJ polypept
45	45	40.2	380	21	AAW90660	Human mutant G pro

ALIGNMENTS

RESULT 1
AAW32476
ID AAW32476 standard; Protein; 166 AA.
XX
AC AAW32476;
XX
DT 15-JAN-1998 (first entry)
XX
DE BCC6 protein for regulating cell death.
XX
KW BCC6 gene; cell death; cell cycle; Bcl2; human.
XX
OS Homo sapiens.
XX
PN US5663316-A.
XX
PD 02-SEP-1997.
XX
PF 18-JUN-1996; 96US-0665617.
XX
PR 18-JUN-1996; 96US-0665617.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Xudong Y;
XX
DR WPI; 1997-447980/41.
XX
DR N-PSDB; AAT91561.
XX
PT Isolated BBC6 gene - encodes a protein that regulates cell death
XX through interaction with Bcl-2
XX
FS Claim 1; Column 11-12; 7pp; English.
XX

CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called Bbc6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the Bbc6 protein in vivo.

XX SQ Sequence 166 AA;

Query Match 100.0%; Score 112; DB 18; Length 166;
 Best Local Similarity 100.0%; Pred. No. 1.5e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAOYRGRELRRMSDEFVD 21
 |||||
 Db 101 nlwaadrygrellrmsdefvd 121

RESULT 2

AAW55779
 ID AAW55779 standard; Protein; 168 AA.

XX AC AAW55779;

XX DT 17-JUL-1998 (first entry)

XX DE Human Bcl-xL/Bcl-2 associated death promoting polypeptide.

XX KW Human; Bcl-xL/Bcl-2 associated death promoting polypeptide; Bad;
 KW programmed cell death; apoptosis.

XX OS Homo sapiens.

XX PN W09812328-A2.

XX PD 26-MAR-1998.

XX PF 18-SEP-1997; 97WO-US16991.

XX PR 20-SEP-1996; 96US-0717123.

XX PA (IDUN-) IDUN PHARM INC.

XX PI Horne WA, Oltersdorf T;

XX PS WPI; 1998-217267/19.

DR N-PSDB; AAV25877.

PT Bad gene mediating apoptosis - used to develop products for treating
 PT e.g. neurodegenerative disease, cancers or autoimmune disease

XX PS Claim 8; Fig 1; 41pp; English.

XX The present sequence is the human Bcl-xL/Bcl-2 associated
 CC death promoting polypeptide, Bad, the binding of which to Bcl-xL
 CC results in the induction of programmed cell death, i.e. apoptosis.
 CC Bad can be used in screening assays for compounds to treat or
 CC prevent diseases characterised by apoptotic cell death, such as
 CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
 CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
 CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
 CC aplastic anaemia and ischaemic injury including myocardial
 CC infarction, stroke and reperfusion injury. Assays can also be
 CC used to obtain apoptosis enhancing compounds to treat or prevent
 CC diseases characterised by the loss of apoptotic cell death, such as
 CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
 CC diseases, e.g. systemic lupus erythematosus and immune-mediated
 CC glomerulonephritis and viral infections, e.g. herpesvirus,
 CC poxvirus or adenovirus infection. Bad can also be used for
 CC detection and diagnosis.

XX SQ Sequence 168 AA;

Query Match 100.0%; Score 112; DB 19; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAOYRGRELRRMSDEFVD 21
 |||||
 Db 103 nlwaadrygrellrmsdefvd 123

RESULT 3

AAAB13512
 ID AAB13512 standard; protein; 168 AA.

XX AC AAB13512;

XX DT 02-NOV-2000 (first entry)

XX DE Human cell proliferation protein APOP-1.

XX KW Human; cell proliferation; APOP-1; cancer; inflammation; infection;
 KW trauma; neurodegenerative disease; ischaemic injury; wasting disease.

XX OS Homo sapiens.

XX PN US6080847-A.

XX PD 27-JUN-2000.

XX PF 04-DEC-1997; 97US-0985335.

XX PR 04-DEC-1997; 97US-0985335.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Corley NC, Hillman JL, Yue H, Lal P, Shah P;

XX PS WPI; 2000-451230/39.

DR N-PSDB; AAA63332.

PT Novel polynucleotide and polypeptide sequences of proteins associated
 PT with cell proliferation for diagnosis, prevention and treatment of e.g.
 PT cancer, acquired immunodeficiency syndrome, and Parkinson's disease

XX PS Example 8; Fig 1; 58pp; English.

XX The present sequence is the human APOP-1 protein. This protein, which
 CC shares structural and chemical homology with Bcl-2, is involved in cell
 CC proliferation. Its coding sequence was isolated by screening a synovial
 CC tissue CDNA library using a computer search for amino acid sequence
 CC alignments. The gene and protein can be used in the treatment of various
 CC cancers, disorders with associated inflammation such as Addison's
 CC disease, adult respiratory distress syndrome, allergies, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, ulcerative colitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, Graves' disease, irritable bowel
 CC syndrome, lupus erythematosus, multiple sclerosis, myasthenia gravis,
 CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
 CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
 CC of cancer, haemodialysis and extracorporeal circulation, infections,
 CC trauma, disorders with associated apoptosis including AIDS and other
 CC infectious and genetic immunodeficiencies, neurodegenerative diseases
 CC such as Alzheimer's disease and Parkinson's disease, ischaemic injuries
 CC such as myocardial infarction, and wasting diseases including cachexia.

XX SQ Sequence 168 AA;

Query Match 100.0%; Score 112; DB 21; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.
 XX
 KW Epitope; murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;
 XX polypeptide; bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
 KW neurodegenerative disease; senescence; ischaemia; neoplasia.
 XX
 OS Mus musculus.
 XX
 PN W09613614-A1.
 XX
 XX 09-MAY-1996.
 PD
 XX 31-OCT-1995; 95WO-US14246.
 XX
 XX 31-OCT-1994; 94US-0333565.
 PR
 XX (UNIW) UNIV WASHINGTON.
 PA
 PI Korsmeyer SJ;
 XX
 XX WPI; 1996-251465/25.
 DR
 XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
 PT useful to treat neoplasia and apoptosis and to identify agents
 PT inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers
 XX
 XX Claim 2; Page 103; 130pp; English.
 XX
 CC The sequences given in AAR95155-67 represent epitopes derived from the
 CC murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see
 CC also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and
 CC bcl-x proteins and regulates cell death. It has homology to the bcl-2-
 CC related family clustered in the BH1 and BH2 domain. Bad has been found
 CC to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in
 CC vivo in mammalian cells. Overexpressed Bad counters the death
 CC inhibitory activity of bcl-x(L), but is much less effective at countering
 CC the death inhibitory activity of bcl-2. Bad expression can accelerate
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
 CC cell line expressing bcl-x(L), and its also counters the death repressor
 CC activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L).
 CC Bad may be used to identify agents which inhibit its binding to bcl-2
 CC or bcl-x(L) to form heterodimers. Such agents may be used to treat
 CC neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
 CC senescence or ischaemia.
 XX
 SQ Sequence 23 AA;

Query Match 91.1%; Score 102; DB 17; Length 23;
 Best Local Similarity 100.0%; Pred. No. 7.7e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
 Db 3 nlwaaqrygrellrmsdef 21

RESULT 7

AAB37001
 ID AAB37001 standard; peptide; 26 AA.
 XX
 AC AAB37001;

XX
 XX 28-FEB-2001 (first entry)
 XX
 XX Bcl2 polypeptide BH3 domain peptide #1.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

KW stroke; myocardial infarction.

XX Homo sapiens.

XX W0200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -
 XX Claim 18; Page 17; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 26 AA;

Query Match 91.1%; Score 102; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 8.8e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
 Db 1 nlwaaqrygrellrmsdef 19

RESULT 8

AAB37002

ID AAB37002 standard; peptide; 26 AA.

XX AAB37002;

XX 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #2.

XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;

KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX Homo sapiens.
 OS WO200059526-A1.
 XX 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US09352.
 PF 07-APR-1999; 99US-0128202.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 DR WPI; 2000-679325/66.
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -
 XX Claim 18; Page 17; 74pp; English.
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX SQ Sequence 26 AA;

Query Match 91.1%; Score 102; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 8.8e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEF 19
 Db 1 nlwaaqrygrellrmsdef 19

RESULT 9
 AAB37003
 ID AAB37003 standard; peptide; 27 AA.
 XX AAB37003;
 XX 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #3.
 DE cardiant; neuroprotective; anti-HIV; virucide; cerebroprotective;
 XX cariant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX Homo sapiens.
 OS WO200059526-A1.
 XX 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US09352.
 PF 07-APR-1999; 99US-0128202.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 DR WPI; 2000-679325/66.
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -
 XX Claim 18; Page 17; 74pp; English.
 CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)n-peptide where n = 1-10; X = C-O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX SQ Sequence 27 AA;

Query Match 91.1%; Score 102; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 9.2e-10;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEF 19
 Db 1 nlwaaqrygrellrmsdef 19

RESULT 10
 AAB37056
 ID AAB37056 standard; peptide; 27 AA.

QY 1 NLWAAQRYGRELRRMSDEF 19
Db 2 nlwaaqrygrellrmsdef 20
|||||

RESULT 12
AAW61319
ID AAW61319 standard; Protein; 59 AA.

XX AC AAW61319;

XX 07-OCT-1998 (first entry)

XX Mutant BCL-XL/BCL-2 associated cell death regulator #4.

XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.

XX OS Mus sp.
OS Synthetic.

XX WO9817682-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US19175.

XX 18-OCT-1996; 96US-0733505.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1998-261422/23.

XX N-PSDB; AAV27837.

PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection

PS Claim 8; Page 73; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.

XX Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.le-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
Db 41 nlwaaqrygrellrmsdef 59
|||||

RESULT 13
AAW61320
ID AAW61320 standard; Protein; 59 AA.

XX AC AAW61320;

XX 07-OCT-1998 (first entry)

XX Mutant BCL-XL/BCL-2 associated cell death regulator #5.

XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.

XX OS Mus sp.
OS Synthetic.

XX WO9817682-A1.

XX 30-APR-1998.

XX 17-OCT-1997; 97WO-US19175.

XX 18-OCT-1996; 96US-0733505.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1998-261422/23.

XX N-PSDB; AAV27838.

PT New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection

PS Claim 8; Page 73; 95pp; English.

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.

XX Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.le-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
| | | | | | | | | | | | | | |
Db 41 nlwaaqrygrelrrmsdef 59

RESULT 14
AAW61321
ID AAW61321 standard; Protein; 59 AA.
XX
AC AAW61321;
XX
DT 07-OCT-1998 (first entry)
XX

DE DE Mutant BCL-XL/BCL-2 associated cell death regulator #6.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX

OS Mus sp.
OS Synthetic.
XX
PN WO9817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX

PI Korsmeyer SJ;
XX

XX WPI: 1998-261422/23.
DR N-PSDB; AAV27839.
XX

XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX

PS Claim 8; Page 73-74; 95pp; English.
XX

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX

SQ Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
| | | | | | | | | | | | | | |
Db 41 nlwaaqrygrelrrmsdef 59

RESULT 15
AAW61322
ID AAW61322 standard; Protein; 59 AA.
XX
AC AAW61322;
XX
DT 07-OCT-1998 (first entry)
XX

DE DE Mutant BCL-XL/BCL-2 associated cell death regulator #7.
XX
KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
KW serine substituted mutant; apoptosis; cancer; viral infection.
XX

OS Mus sp.
OS Synthetic.
XX
PN WO9817682-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US19175.
XX
PR 18-OCT-1996; 96US-0733505.
XX
PA (UNIW) UNIV WASHINGTON.
XX

PI Korsmeyer SJ;
XX

XX WPI: 1998-261422/23.
DR N-PSDB; AAV27840.
XX

XX New mutant BAD polypeptide with phosphorylatable serine replaced -
PT useful for, e.g. treating reduced apoptosis such as in cancer or
PT viral infection
XX

PS Claim 24; Page 74; 95pp; English.
XX

XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
CC death regulator) proteins, having an amino acid other than Ser at
CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
CC present sequence represents a mutant BAD protein. Also described are: (1)
CC fragments of mutant BAD protein able to decrease cell viability; (2)
CC fusion proteins of mutant BAD with a heterologous polypeptide that
CC increases intracellular delivery. Mutant BAD proteins are used to treat
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
CC viral infection, lymphoproliferation, arthritis, infertility,
CC inflammation and autoimmune disease. Polynucleotide sequences encoding
CC mutant BAD proteins can be used similarly by gene therapy or to produce
CC transgenic animals for use as disease models or in drug screening. BAD
CC proteins phosphorylated at specified Ser are used to screen for enhancers
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
CC aging or ischaemic cell death. The apoptotic status of cells is
CC determined by measuring relative amounts of phosphorylated and non-
CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
CC greater death-promoting activity than wild-type BAD which can become
CC phosphorylated on the specified Ser, forming a product that does not
CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
CC proteins in the cytosol, thus promoting cell survival. The mutants with
CC Ser substituted cannot bind 14-3-3.
XX

SQ Sequence 59 AA;

Query Match 91.1%; Score 102; DB 19; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 NLWAAQRYGRELRMSDEF 19
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Db 41 nlwaaqrygreLRMSdef 59

Search completed: October 9, 2001, 15:53:27
Job time: 203 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 16:07:48 ; Search time 239.36 seconds
(without alignments)
19.464 Million cell updates/sec

Title: US-09-580-523-1_COPY_103_123
Sequence: 1 NLWAAQRYGRELRRMSDEVD 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues
Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	100.0	21	US-09-580-523-1_COPY_103_123	Sequence 30, Appl
2	112	100.0	21	US-09-580-523-1_COPY_103_123	Sequence 30, Appl
3	112	100.0	21	US-09-580-523-1_COPY_103_123	Sequence 36, Appl
4	112	100.0	22	US-09-580-523-1_COPY_103_123	Sequence 29, Appl
5	112	100.0	22	US-09-580-523-1_COPY_103_123	Sequence 29, Appl
6	112	100.0	23	US-09-580-523-1_COPY_103_123	Sequence 28, Appl
7	112	100.0	23	US-09-580-523-1_COPY_103_123	Sequence 28, Appl
8	112	100.0	24	US-09-580-523-1_COPY_103_123	Sequence 27, Appl
9	112	100.0	24	US-09-580-523-1_COPY_103_123	Sequence 27, Appl
10	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 10, Appl

11	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 17, Appl
12	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 18, Appl
13	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 19, Appl
14	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 20, Appl
15	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 16, Appl
16	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 17, Appl
17	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 18, Appl
18	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 19, Appl
19	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 20, Appl
20	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 20, Appl
21	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 26, Appl
22	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 27, Appl
23	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 28, Appl
24	112	100.0	25	US-09-580-523-1_COPY_103_123	Sequence 29, Appl
25	112	100.0	63	US-09-580-523-1_COPY_103_123	Sequence 12, Appl
26	112	100.0	63	US-09-580-523-1_COPY_103_123	Sequence 42, Appl
27	112	100.0	125	US-09-580-523-1_COPY_103_123	Sequence 42, Appl
28	112	100.0	125	US-09-580-523-1_COPY_103_123	Sequence 1338, A
29	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 1, Appl
30	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 2, Appl
31	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 2, Appl
32	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 2, Appl
33	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 1, Appl
34	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 7, Appl
35	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 1, Appl
36	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 32, Appl
37	112	100.0	168	US-09-580-523-1_COPY_103_123	Sequence 21, Appl
38	108	96.4	21	US-09-580-523-1_COPY_103_123	Sequence 7, Appl
39	108	96.4	21	US-09-580-523-1_COPY_103_123	Sequence 7, Appl
40	108	96.4	25	US-09-580-523-1_COPY_103_123	Sequence 15, Appl
41	108	96.4	25	US-09-580-523-1_COPY_103_123	Sequence 16, Appl
42	108	96.4	25	US-09-580-523-1_COPY_103_123	Sequence 15, Appl
43	108	96.4	25	US-09-580-523-1_COPY_103_123	Sequence 16, Appl
44	108	96.4	25	US-09-580-523-1_COPY_103_123	Sequence 24, Appl
45	108	96.4	25	US-09-580-523-1_COPY_103_123	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-580-523-1_COPY_103_123

; Sequence 30, Application US/0956399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Fesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, Shichung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370-US.OI
; CURRENT APPLICATION NUMBER: US/09/566,399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: wild-type human BAB peptide
US-09-580-523-1_COPY_103_123

Query Match 100.0% Score 112; DB 20; Length 21;

; OTHER INFORMATION: synthetic peptide
US-09-656-399A-29

Query Match 100.0%; Score 112; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 6

US-09-656-399-28
; Sequence 28, Application US/09656399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Fesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, Shichung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Wild-type human BAD peptide
US-09-656-399-28

Query Match 100.0%; Score 112; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 7

US-09-656-399A-28
; Sequence 28, Application US/09656399A
; GENERAL INFORMATION:
; APPLICANT: Fesik, Stephen F.
; APPLICANT: Meadows, Robert P.
; APPLICANT: Joseph, Mary K.
; APPLICANT: Olejniczak, Edward T.
; APPLICANT: Petros, Andrew M.
; APPLICANT: Nettesheim, David G.
; APPLICANT: Swift, Kerry M.
; APPLICANT: Matayoshi, Edmund
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6730.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399A
; CURRENT FILING DATE: 2000-09-06

; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-656-399A-28

Query Match 100.0%; Score 112; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 8

US-09-656-399-27
; Sequence 27, Application US/09656399
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Fesik, Steven
; APPLICANT: Petros, Andrew
; APPLICANT: Nettesheim, David
; APPLICANT: Meadows, Bob
; APPLICANT: Olejniczak, Ed
; APPLICANT: Zhang, Haichao
; APPLICANT: Ng, Shichung
; APPLICANT: Swift, Kerry
; APPLICANT: Matayoshi, Ed
; APPLICANT: Joseph, Mary K.
; TITLE OF INVENTION: MUTANT PEPTIDES DERIVED FROM BAD AND
; TITLE OF INVENTION: THEIR USE TO IDENTIFY SUBSTANCES WHICH BIND TO A MEMBER OF
; TITLE OF INVENTION: THE BCL-2 FAMILY OF PROTEINS
; FILE REFERENCE: 6370.US.01
; CURRENT APPLICATION NUMBER: US/09/656,399
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Wild-type human BAD peptide
US-09-656-399-27

Query Match 100.0%; Score 112; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 1 NLWAAQRYGRELRRMSDEFVD 21

RESULT 9

US-09-656-399A-27
; Sequence 27, Application US/09656399A
; GENERAL INFORMATION:
; APPLICANT: Fesik, Stephen F.
; APPLICANT: Meadows, Robert P.
; APPLICANT: Joseph, Mary K.
; APPLICANT: Olejniczak, Edward T.
; APPLICANT: Petros, Andrew M.
; APPLICANT: Nettesheim, David G.
; APPLICANT: Swift, Kerry M.
; APPLICANT: Matayoshi, Edmund

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:55:20 ; Search time 17.79 Seconds
(without alignments)
40.436 Million cell updates/sec

Title: US-09-580-523-1_COPY_103_123
Perfect score: 112
Sequence: 1 NLWAAQRYGRELRRMSDEFVD 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	168	1	BAD_HUMAN
2	102	91.1	204	1	BAD_MOUSE
3	47.5	42.4	595	1	VGL1_BPMD2
4	46.5	41.5	503	1	MTBR_BPRH1
5	45	40.2	287	1	PRFA_POLPE
6	45	40.2	370	1	AROG_YEAST
7	45	40.2	377	1	APJ_MOUSE
8	45	40.2	380	1	APJ_HUMAN
9	45	40.2	380	1	APJ_MACMU
10	44	39.3	1008	1	DPOL_HSV2
11	43	38.4	220	1	6PGL_THENA
12	43	38.4	370	1	AROG_CANAL
13	43	38.4	463	1	Y030_NPVAC
14	43	38.4	905	1	Z03_MOUSE
15	43	38.4	1557	1	LMML_CAEEL
16	42	37.5	185	1	RRF_THEMEA
17	42	37.5	432	1	TIG_ECOLI
18	42	37.5	501	1	TDT_ONCMY
19	42	37.5	653	1	HT2A_HUMAN
20	42	37.5	715	1	DCLY_SALTY
21	42	37.5	752	1	NECL_RAT
22	41	36.6	391	1	UBIF_ECOLI
23	41	36.6	629	1	DNAK_HALCU
24	41	36.6	704	1	KPCI_CAEEL
25	41	36.6	861	1	GCR3_YEAST
26	41	36.6	883	1	CAPP_ECOLI
27	41	36.6	4466	1	DYHC_ANTCR
28	40.5	36.2	143	1	YXAD_BACSU
29	40.5	36.2	659	1	YYBT_BACSU
30	40	35.7	188	1	ADML_BOVIN
31	40	35.7	205	1	TENI_BACSU
32	40	35.7	261	1	YGFQ_ECOLI
33	40	35.7	380	1	PHLC_TRYCR

34	40	35.7	494	1	CAT2_HORVU	P55308 hordeum vul
35	40	35.7	578	1	ACEK_ECOLI	P11071 escherichia
36	40	35.7	583	1	ACEK_SALTY	P51067 salmonella
37	40	35.7	631	1	RPSD_BORBU	P52323 borrelia bu
38	39	34.8	125	1	VSIS_REOVJ	P32868 reovirus (t
39	39	34.8	185	1	ADML_HUMAN	P33318 homo sapien
40	39	34.8	282	1	HBD_CLOAB	P52041 clostridium
41	39	34.8	312	1	CELF_PVRKA	O85230 pseudorabie
42	39	34.8	331	1	OTCC_NEIMA	O91c14 neisseria m
43	39	34.8	331	1	OTCC_NEIMA	O91y13 neisseria m
44	39	34.8	365	1	RA51_SCHPO	P36601 schizosacch
45	39	34.8	418	1	VS12_REOVD	P03525 reovirus (t

ALIGNMENTS

RESULT 1
BAD_HUMAN
ID BAD_HUMAN STANDARD; PRT; 168 AA.
AC Q92934;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
GN BAD OR BBC6 OR BCL2L8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin D.X., Li Z., Huang B., Chen S., Zhou H.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE
CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL
CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2
CC (BY SIMILARITY).
CC -I- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
CC BAX, MCL-1, A1, OR BCL-X(S) (BY SIMILARITY).
CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -I- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -I- SIMILARITY: CONTAINS A BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL; U66879; AAB36516.1; -
DR MIM; 603167; -
KW Apoptosis.
FT DOMAIN 101 121 BH1.
FT DOMAIN 146 163 BH2.
SQ SEQUENCE 168 AA; 18408 MW; BDF3D99587C222BE CRC64;
Query Match 100.0%; Score 112; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
|||||
DB 103 NLWAAQRYGRELRRMSDEFVD 123
RESULT 2
BAD_MOUSE

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ID BAD_MOUSE STANDARD; PRT; 204 AA.
AC Q61337;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BAD PROTEIN (BCL-2 BINDING COMPONENT 6).
GN BAD OR BCL-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Thymus;
RX MEDLINE=95136361; PubMed=7834748;
RA Yang E., Zha J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;
RT "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
RT promotes cell death.";
RL Cell 80:285-291(1995).
CC -1- FUNCTION: PROMOTES CELL DEATH. SUCCESSFULLY COMPETES FOR THE
CC BINDING TO BCL-X(L) AND BCL-2, THEREBY AFFECTING THE LEVEL
CC HETERODIMERIZATION OF BOTH THESE PROTEINS WITH BAX. CAN REVERSE
CC THE DEATH REPRESSOR ACTIVITY OF BCL-X(L), BUT NOT THAT OF BCL-2.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-X(L) AND BCL-2, BUT NOT WITH
CC BAX, MCL-1, AL, OR BCL-X(S).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
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CC
CC EMBL; L37296; AAA64465.1; -.
CC DR EMBL; L37296; AAA64465.1; -.
CC DR MGD; MGI:1096330; Bad.
CC KW Apoptosis.
FT DOMAIN 138 158 BH1.
FT DOMAIN 182 199 BH2.
SQ SEQUENCE 204 AA; 22080 MW; 6C2BA910205053F7 CRC64;

Query Match 91.1%; Score 102; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
Db 140 NLWAAQRYGRELRRMSDEF 158

RESULT 3
VG13_BPMD2 STANDARD; PRT; 595 AA.
ID VG13_BPMD2
AC O64206;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENE 13 PROTEIN (GP13).
GN 13.
OS Mycobacteriophage D29.
OC Viruses.
OX NCBI_TaxID=28369;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98300335; PubMed=9636706;
RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
RT "Genome structure of mycobacteriophage D29: implications for phage
RT evolution.";
RL J. Mol. Biol. 279:143-164(1998).

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CC
CC EMBL; AF022214; AAC18453.1; -.
CC DR EMBL; AF022214; AAC18453.1; -.
CC SQ SEQUENCE 595 AA; 66397 MW; AFD123ED5371E263 CRC64;

Query Match 42.4%; Score 47.5; DB 1; Length 595;
Best Local Similarity 47.6%; Pred. No. 5.5;
Matches 10; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
Db 435 DIWDPQKYGGEVPR---EFVD 452

RESULT 4
MTBR_BPRH1 STANDARD; PRT; 503 AA.
ID MTBR_BPRH1
AC P09915;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MODIFICATION METHYLASE RHO11SI (EC 2.1.1.73) (CYTOSINE-SPECIFIC
DE METHYLTRANSFERASE RHO11SI) (BSU P11S) (M.RHO11SI).
OS Bacteriophage rho-11s.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC Lambda phage group.
OX NCBI_TaxID=10735;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87246516; PubMed=3109889;
RA Behrens B., Noyer-Weidner M., Pawlek B., Lauster R., Balganesch T.S.,
RA Trautner T.A.;
RT "Organization of multispecific DNA methyltransferases encoded by
RT temperate Bacillus subtilis phages.";
RL EMBO J. 6:1137-1142(1987).
RN [2]
RP REVISION TO 476.
RA Trautner T.A.;
RL Submitted (SEP-1987) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS ENZYME METHYLATES CYTOSINE WITHIN THE SEQUENCES
CC GGCC AND GAGCTC.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE =
CC S-ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
CC -1- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X05242; CAA28869.1; -.
CC DR EMBL; X05242; CAA28869.1; -.
CC DR PIR; A28137; CTBPRH.
CC DR HSSP; P05102; 5MHT.
CC DR REBASE; 2835; M.Rho11SI.
CC DR InterPro; IPR001525; -.
CC DR Pfam; PF00145; DNA_methylase; 1.
CC DR PRINTS; PR00105; C5METTRFAS.
CC DR PROSITE; PS00094; C5_MTASE_1; 1.
CC DR PROSITE; PS00095; C5_MTASE_2; 1.
CC DR TRANSFERASE; Methyltransferase; Restriction system.
CC ACT_SITE 78 78
CC FT ACT_SITE 78 78 BY SIMILARITY.
CC SQ SEQUENCE 503 AA; 57129 MW; AAAPB8FE01B8129E CRC64;

```

FT	MOD_RES	53	53	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	59	59	AMIDATION (G-60 PROVIDE AMIDE GROUP)
FT	MOD_RES	65	65	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	71	71	AMIDATION (G-72 PROVIDE AMIDE GROUP)
FT	MOD_RES	78	78	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	84	84	AMIDATION (G-85 PROVIDE AMIDE GROUP)
FT	MOD_RES	91	91	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	97	97	AMIDATION (G-98 PROVIDE AMIDE GROUP)
FT	MOD_RES	104	104	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	110	110	AMIDATION (G-111 PROVIDE AMIDE GROUP)
FT	MOD_RES	117	117	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	123	123	AMIDATION (G-124 PROVIDE AMIDE GROUP)
FT	MOD_RES	130	130	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	136	136	AMIDATION (G-137 PROVIDE AMIDE GROUP)
FT	MOD_RES	143	143	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	149	149	AMIDATION (G-150 PROVIDE AMIDE GROUP)
FT	MOD_RES	169	169	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	175	175	AMIDATION (G-176 PROVIDE AMIDE GROUP)
FT	MOD_RES	182	182	PYRROLIDONE CARBOXYLIC ACID
FT	MOD_RES	188	188	AMIDATION (G-189 PROVIDE AMIDE GROUP)
FT	MOD_RES	195	195	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	201	201	AMIDATION (G-202 PROVIDE AMIDE GROUP)
FT	MOD_RES	208	208	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	214	214	AMIDATION (G-215 PROVIDE AMIDE GROUP)
FT	MOD_RES	221	221	PYRROLIDONE CARBOXYLIC ACID (POTENTIAL)
FT	MOD_RES	227	227	AMIDATION (G-228 PROVIDE AMIDE GROUP)
SEQ	SEQUENCE	287	33531 MW; FDFIF52C47D4BB11 CRC64;	

Query Match 40.2%; Score 45; DB 1; Length 287;
Best Local Similarity 33.3%; Pred. No. 6.1;
Matches 10; Conservative 5; Mismatches 5; Indels 10; Gaps

QY	1 NLWAAQRYGREL-----RMSDEFV 20	
DB	64 NQWLKGRFGRELSQWLKGRFGRELSQWL 93	

RESULT 6

ID	AROG_YEAST	STANDARD;	PRT;	370 AA.
AC	P32449;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	PHOSHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED			
DE	(EC 4.1.2.15) (PHOSHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE) (DAHP			
DE	SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE).			
GN	AR04 O YBR249C OR YBR1701.			
OC	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
OX	NCBI_TaxID=4932;			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RP	MEDLINE=9225349; PubMed=1348717;			
RT	Kuenzler M., Paravicini G., Egli C., Irmiger S., Braus G.H.;			
RT	"Cloning, primary structure and regulation of the ARO4 gene, encoding			
RT	the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate 7-phosphate			
RT	synthase from <i>Saccharomyces cerevisiae</i> ."			
RL	Gene 113:67-74(1992).			
RN	[2]			
RP	REVISIONS TO 205-207.			
RA	Kuenzler M.;			
RL	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=S288C;			
RX	MEDLINE=94078675; PubMed=8256522;			
RT	Daignon F., Bileau N., Aigle M., Crouzet M.;			
RT	"The complete sequence of a 6794 bp segment located on the right arm			
RT	of chromosome II of <i>Saccharomyces cerevisiae</i> . Finding of a putative			
RT	dUTPase in a yeast."			

```

RL Yeast 9:1131-1137(1993).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
CC -1- CATALYTIC ACTIVITY: 7-PHOSPHO-2-DEHYDRO-3-DEOXY-D-ARABINO-
CC HEPTONATE + ORTHOPHOSPHATE = PHOSPHOENOLPYRUVATE + D-ERYTHROSE
CC 4-PHOSPHATE + H(2)O.
CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE.
CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
CC -1- INDUCTION: BY AMINO ACID STARVATION.
CC -1- SIMILARITY: BELONGS TO CLASS-I DAHP SYNTHETASE FAMILY.
CC
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CC
CC EMBL; X61107; CAA43419.1; -
CC EMBL; L20296; AAA65607.1; -
CC EMBL; Z36118; CAA85212.1; -
CC PIR; S38185; S38185.
CC SGD; S0000453; ARO4.
CC InterPro; IPR001785; -
CC Pfam; PF00793; DAHP_synth.1; 1.
CC Aromatic amino acid biosynthesis; Lyase; Multigene family.
KW SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
SQ

```

Query Match 40.2%; Score 45; DB 1; Length 370;
Best Local Similarity 50.0%; Pred. No. 8;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

```

QY 1 NLWAAQRYGRELRRMSDE 18
DB 80 DLEAAQAEYALRLAKLSDE 97

```

RESULT 7
APJ_MOUSE
ID APJ_MOUSE STANDARD; PRT; 377 AA.
AC Q9WV08;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (MSR).
GN AGTRL1 OR APJ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA Rizzotti K.;
RT "The G protein-coupled receptor msr/APJ is expressed in endothelial precursors";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; X61107; CAA43419.1; -
CC EMBL; L20296; AAA65607.1; -
CC EMBL; Z36118; CAA85212.1; -
CC PIR; S38185; S38185.
CC SGD; S0000453; ARO4.
CC InterPro; IPR001785; -
CC Pfam; PF00793; DAHP_synth.1; 1.
CC Aromatic amino acid biosynthesis; Lyase; Multigene family.
KW SEQUENCE 370 AA; 39749 MW; 594ED48F24175979 CRC64;
SQ

Query Match 40.2%; Score 45; DB 1; Length 377;
Best Local Similarity 47.4%; Pred. No. 8.2;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

QY 2 LWAAQRYGRELRRMSDEFV 20
DB 48 LMTVFTSREKRRSADIFI 66

```

RESULT 8
APJ_HUMAN
ID APJ_HUMAN STANDARD; PRT; 380 AA.
AC P35414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
GN AGTRL1 OR APJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94124031; PubMed=8294032;
RA O'Dowd B.F., Heiber M., Chan A., Heng H.H., Tsui L.-C., Kennedy J.L.,
RA Shi X., Petronis A., George S.R., Nguyen T.;
RT "A human gene that shows identity with the gene encoding the angiotensin receptor is located on chromosome 11";
RL Gene 136:355-360(1993).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ007612; CAB50696.1; -
CC MGD; MGI:1346086; Agtr1l.
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS02662; G-PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 49 1 (POTENTIAL).
FT DOMAIN 50 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 89 2 (POTENTIAL).
FT DOMAIN 90 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 123 3 (POTENTIAL).
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 164 4 (POTENTIAL).
FT DOMAIN 165 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).
FT DOMAIN 220 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 269 6 (POTENTIAL).
FT DOMAIN 270 282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 283 306 7 (POTENTIAL).
FT DOMAIN 307 377 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 377 AA; 42266 MW; AA437A800A24E0B CRC64;

Query Match 40.2%; Score 45; DB 1; Length 377;
Best Local Similarity 47.4%; Pred. No. 8.2;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

QY 2 LWAAQRYGRELRRMSDEFV 20
DB 48 LMTVFTSREKRRSADIFI 66

```

RESULT 8
APJ_HUMAN
ID APJ_HUMAN STANDARD; PRT; 380 AA.
AC P35414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
GN AGTRL1 OR APJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94124031; PubMed=8294032;
RA O'Dowd B.F., Heiber M., Chan A., Heng H.H., Tsui L.-C., Kennedy J.L.,
RA Shi X., Petronis A., George S.R., Nguyen T.;
RT "A human gene that shows identity with the gene encoding the angiotensin receptor is located on chromosome 11";
RL Gene 136:355-360(1993).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AJ007612; CAB50696.1; -
CC MGD; MGI:1346086; Agtr1l.
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS02662; G-PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
KW DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 49 1 (POTENTIAL).
FT DOMAIN 50 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 89 2 (POTENTIAL).
FT DOMAIN 90 98 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 99 123 3 (POTENTIAL).
FT DOMAIN 124 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 164 4 (POTENTIAL).
FT DOMAIN 165 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 219 5 (POTENTIAL).
FT DOMAIN 220 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 269 6 (POTENTIAL).
FT DOMAIN 270 282 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 283 306 7 (POTENTIAL).
FT DOMAIN 307 377 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 377 AA; 42266 MW; AA437A800A24E0B CRC64;

Query Match 40.2%; Score 45; DB 1; Length 377;
Best Local Similarity 47.4%; Pred. No. 8.2;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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```
CC EMBL; U03642; AAA18954.1; -
CC GCRdb; GCR_0806; -
CC MIM; 600052; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC KW DOMAIN 1 26
CC EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 27 51
CC DOMAIN 52 66
CC TRANSMEM 67 91
CC DOMAIN 92 100
CC TRANSMEM 101 125
CC DOMAIN 126 144
CC TRANSMEM 145 166
CC DOMAIN 167 200
CC TRANSMEM 201 221
CC DOMAIN 222 244
CC TRANSMEM 245 271
CC DOMAIN 272 284
CC TRANSMEM 285 308
CC DOMAIN 309 380
CC TRANSMEM 380 AA; 42660 MW; 76DB18BEA6D2B2E4 CRC64;
CC SEQUENCE 380 AA; 42660 MW; 76DB18BEA6D2B2E4 CRC64;
CC
CC Query Match 40.2%; Score 45; DB 1; Length 380;
CC Best Local Similarity 47.4%; Pred. No. 8.3;
CC Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
CC
CC Qy 2 LWAQRYGRELRRMSDEFV 20
CC || | | | | | | | |
CC Db 50 LWTVFRSSREKRRSADIFI 68
CC
CC RESULT 9
CC APJ_MACMU STANDARD; PRT; 380 AA.
CC AC O97666;
CC DT 01-OCT-2000 (Rel. 40, Created)
CC DT 01-OCT-2000 (Rel. 40, Last sequence update)
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC DE PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
CC GN AGTRL1 OR APJ.
CC OS Macaca mulatta (Rhesus macaque).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC OC Cercopithecinae; Macaca.
CC OX NCBI_TaxID=9544;
CC [1]
CC RN SEQUENCE FROM N.A.
CC RC TISSUE-Spleen;
CC RA Margulies B.J., Haver D.A., Clements J.E.;
CC RT "Identification and characterization of thirteen rhesus macaque
CC chemokine receptors and chemokine receptor homologues.";
CC RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: ORPHAN RECEPTOR.
CC CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC -1- HIGHLY RELATED TO ANGIOTENSIN-RECEPTOR 1.
CC
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CC EMBL; AF100206; AAC72404.1; -
CC InterPro; IPR000276; -
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC KW DOMAIN 1 26
CC EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 27 51
CC DOMAIN 52 66
CC TRANSMEM 67 91
CC DOMAIN 92 100
CC TRANSMEM 101 125
CC DOMAIN 126 144
CC TRANSMEM 145 166
CC DOMAIN 167 200
CC TRANSMEM 201 221
CC DOMAIN 222 244
CC TRANSMEM 245 271
CC DOMAIN 272 284
CC TRANSMEM 285 308
CC DOMAIN 309 380
CC TRANSMEM 380 AA; 42606 MW; E84F03E31FABF7ED CRC64;
CC SEQUENCE 380 AA; 42606 MW; E84F03E31FABF7ED CRC64;
CC
CC Query Match 40.2%; Score 45; DB 1; Length 380;
CC Best Local Similarity 47.4%; Pred. No. 8.3;
CC Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
CC
CC Qy 2 LWAQRYGRELRRMSDEFV 20
CC || | | | | | | | |
CC Db 50 LWTVFRSSREKRRSADIFI 68
CC
CC RESULT 10
CC DPOL_HSVE2 STANDARD; PRT; 1008 AA.
CC AC P52367;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE DNA POLYMERASE (EC 2.7.7.7).
CC GN 9.
CC OS Equine herpesvirus type 2 (strain 86/87) (EHV-2).
CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC OC Gammaherpesvirinae.
CC OX NCBI_TaxID=82831;
CC [1]
CC RN SEQUENCE FROM N.A.
CC RP MEDLINE-95302501; PubMed-7783207;
CC RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
CC RT "The DNA sequence of equine herpesvirus 2.";
CC RL J. Mol. Biol. 249:520-528(1995).
CC CC -1- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
CC N PYROPHOSPHATE + DNA(N).
CC CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
CC
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RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
RT polyhedrosis virus.";
RL Virology 202:586-605(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=95079853; PubMed=1333113;
RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
RA Summers M.D.;
RT "Sequence, genomic organization of the EcoRI-A fragment of Autographa
RT californica nuclear polyhedrosis virus, and identification of a
RT viral-encoded protein resembling the outer capsid protein VP8 of
RT rotavirus.";
RL Virology 191:1003-1008(1992).
CC -1- SIMILARITY: TO CORRESPONDING ORF IN OPNPV.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 294
CC ONWARD AND IS SHORTER (354 AA) DUE TO A FRAMESHIFT.
CC -----
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CC -----
CC EMBL; L22858; AAA66660.1; -
CC EMBL; M96361; AAA66798.1; ALT_FRAME.
CC PIR; F36828; F36828.
CC Hypothetical protein.
CC CONFLICT 254 262 AYYIRHMF -> GTTLDTCLL (IN REF. 2).
CC SEQUENCE 463 AA; 54688 MW; D3643E87E2C6D373 CRC64;
CC -----
Query Match 38.4%; Score 43; DB 1; Length 463;
Best Local Similarity 55.08; Pred. No. 21;
Matches 11; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

Qy 2 LWAAQRYGRELRLMSDFVD 21
||| ||| | ||| |
Db 347 LWKA--YGRHLKNSDECDD 364

RESULT 14
Z03_MOUSE
ID Z03_MOUSE STANDARD; PRT; 905 AA.
AC Q90XY1;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TIGHT JUNCTION PROTEIN ZO-3 (ZONA OCCLUDENS 3 PROTEIN) (TIGHT JUNCTION
DE PROTEIN 3).
GN TJP3 OR ZO3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20069797; PubMed=10601346;
RA Itoh M., Furuse M., Morita K., Kubota K., Saitou M., Tsukita S.;
RT "Direct binding of three tight junction-associated MAGUKs, ZO-1, ZO-2,
RT and ZO-3, with the COOH termini of claudins.";
RL J. Cell Biol. 147:1351-1363(1999).
CC -1- SUBUNIT: INTERACTS WITH OCCLUDIN, CLAUDINS AND ZO-1.
CC -1- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -1- SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN.
```

```
CC -1- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -----
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CC -----
CC EMBL; AF157006; AAF24175.1; -
CC HSSP; P31016; IBFE.
CC MGD; MG1:1351650; Tjp3.
CC InterPro; IPR000619; -
CC InterPro; IPR001478; -
CC Pfam; PF00595; PDZ; 3.
CC Pfam; PF00625; Guanylate_kin; 1.
CC PROSITE; PS00856; GUANYLATE_KINASE_1; FALSE_NEG.
CC PROSITE; PS00502; GUANYLATE_KINASE_2; 1.
CC PROSITE; PS0106; PDZ; 3.
CC Tight junction; SH3 domain; Repeat; Membrane.
CC FT DOMAIN 11 93
CC FT DOMAIN 187 264 PDZ 1.
CC FT DOMAIN 368 434 PDZ 3.
CC FT DOMAIN ? ? SH3.
CC FT DOMAIN 654 754 GUANYLATE KINASE.
CC SQ SEQUENCE 905 AA; 99324 MW; B787BA1592661FEE CRC64;
CC -----
Query Match 38.4%; Score 43; DB 1; Length 905;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LWAAQRYGRELRL 13
||| | ||| |
Db 513 LWLAARMGRDLR 524

RESULT 15
LWML_CAEEL
ID LWML_CAEEL STANDARD; PRT; 1557 AA.
AC Q18823;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LAMININ-LIKE PROTEIN C54D1.5 PRECURSOR.
GN C54D1.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Minx P.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -1- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
CC -----
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CC -----
CC EMBL; U46673; AAC48152.1; -
CC HSSP; P02468; ITLE.
CC WormPep; C54D1.5; CE06981.
CC InterPro; IPR000034; -
CC InterPro; IPR000561; -
```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:56 ; Search time 46.39 Seconds
(without alignments)
59.892 Million cell updates/sec

Title: US-09-580-523-1_COPY_103_123

Perfect score: 112

Sequence: 1 NLWAAQRYGRELRRMSDEFVD 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phase:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-unclassified:*
- 13: sp-vertebrate:*
- 14: sp-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	168	4	014803
2	102	91.1	205	11	035147
3	102	91.1	205	11	070256
4	102	91.1	220	11	09JHX1
5	82	73.2	95	13	09I9N2
6	53	47.3	223	2	Q10843
7	49	43.8	453	2	Q91403
8	49	43.8	1248	2	Q9HZ03
9	47	42.0	295	2	Q9HY62
10	47	42.0	339	10	Q9F005
11	46.5	41.5	486	5	Q9VVM1
12	46	41.1	198	4	Q43521
13	45	40.2	564	2	Q9RUK9
14	45	40.2	574	2	Q69125
15	45	40.2	848	5	Q94419
16	45	40.2	1303	5	Q9U172
17	44	39.3	226	5	Q44466
18	44	39.3	335	10	Q64692
19	44	39.3	516	10	Q9SSP5

20	43.5	38.8	503	9	Q02778
21	43	38.4	156	2	Q9JTL8
22	43	38.4	186	2	Q9X5V5
23	43	38.4	232	2	Q24956
24	43	38.4	232	2	Q87194
25	43	38.4	232	2	Q9ZMT5
26	43	38.4	276	10	Q9FJV5
27	43	38.4	302	13	Q12968
28	43	38.4	314	2	Q9F2J4
29	43	38.4	325	2	Q07600
30	43	38.4	363	10	Q9LWN7
31	43	38.4	375	2	Q9L395
32	43	38.4	463	14	Q9JAD7
33	43	38.4	472	14	Q92397
34	43	38.4	5635	5	Q9N9N1
35	42	37.5	196	11	Q54918
36	42	37.5	196	11	Q88498
37	42	37.5	202	2	Q9I3G1
38	42	37.5	361	10	Q9FIC1
39	42	37.5	415	5	Q9V7Y6
40	42	37.5	461	2	Q9KR33
41	42	37.5	519	8	Q9WT28
42	42	37.5	520	4	Q9H239
43	42	37.5	525	10	Q39144
44	42	37.5	526	10	Q9S7B5
45	42	37.5	548	2	P71029

ALIGNMENTS

RESULT 1

014803 PRELIMINARY; PRT; 168 AA.

AC 014803;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE BCL-X/BCL-2 BINDING PROTEIN (FRAGMENT).

GN BAD.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97083574; PubMed=8929532;

RA Wang H.G., Rapp U.R., Reed J.C.;

RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria.";

RL Cell 87:629-638(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Takayama S., Reed J.C.;

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Otilie S., Diaz J.L., Horne W., Chang J., Wang Y., Wilson G., Weeks S., McConnell M., Chang S., Fritz L.C., Oltersdorf T., J. Biol. Chem. 0:0-0(1997).

DR EMBL; AF021792; AAB72092.1; -.

DR EMBL; AF031523; AAB88124.1; -.

FT NON_TER 1

SQ SEQUENCE 168 AA; 18392 MW; 69FD8D27DDEE3241 CRC64;

Query Match 100.0%; Score 112; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLWAAQRYGRELRRMSDEFVD 21
DB 103 NLWAAQRYGRELRRMSDEFVD 123

```
RESULT 2
Q35147 ID Q35147 PRELIMINARY; PRT; 205 AA.
AC Q35147;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER.
GN BAD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=98034386; PubMed=9369453;
RZ Hsu S.Y., Hsueh A.J.W.;
RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
RT apoptosis in mammalian cells by 14-3-3 isoforms and P11.";
RL Mol. Endocrinol. 11:1858-1867(1997).
DR EMBL; AF003523; AAC53374.1; -.
SQ SEQUENCE 205 AA; 22468 MW; 04DD3E8A03B11168 CRC64;

Query Match 91.1%; Score 102; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 9.5e-08; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||
Db 141 NLWAAQRYGRELRRMSDEF 159

RESULT 3
O70256 ID O70256 PRELIMINARY; PRT; 205 AA.
AC O70256;
DT 01-AUG-1998 (TEMBLrel. 07, Created)
DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH PROMOTER BAD (BCL-2 ASSOCIATED DEATH AGONIST
DE ALPHA).
GN BAD OR BAD-ALPHA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98194755; PubMed=9535132;
RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator Bad in
RT the rat brain.";
RL Neurosci. Lett. 243:137-140(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031227; AAC15100.1; -.
DR EMBL; AF279910; AAF91427.1; -.
SQ SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9CF4A81 CRC64;

Query Match 91.1%; Score 102; DB 11; Length 205;
Best Local Similarity 100.0%; Pred. No. 9.5e-08; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||
Db 141 NLWAAQRYGRELRRMSDEF 159

Query Match 91.1%; Score 102; DB 11; Length 220;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||
Db 141 NLWAAQRYGRELRRMSDEF 159

RESULT 4
Q9JHX1 ID Q9JHX1 PRELIMINARY; PRT; 220 AA.
AC Q9JHX1;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE BCL-2 ASSOCIATED DEATH AGONIST BETA.
GN BAD-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamner S., Arumne U., Li-Ying Y., Sun Y.-F., Saarma M., Lindholm D.;
RT "Functional characterization of two splice variants of rat bad and
RT their interaction with bcl-w in sympathetic neurons.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279911; AAF91428.1; -.
SQ SEQUENCE 220 AA; 24278 MW; E27BCCD7C969E90F CRC64;

Query Match 91.1%; Score 102; DB 11; Length 220;
Best Local Similarity 100.0%; Pred. No. 1e-07; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 NLWAAQRYGRELRRMSDEF 19
|||||
Db 141 NLWAAQRYGRELRRMSDEF 159

RESULT 5
Q9I9N2 ID Q9I9N2 PRELIMINARY; PRT; 95 AA.
AC Q9I9N2;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE BAD (FRAGMENT).
GN BAD.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Inohara N., Nunez G.;
RT "Genes with Homology to Mammalian Apoptosis Regulators Identified in
RT Zebrafish.";
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF231017; AAF66962.1; -.
FT NON_TER 1
SQ SEQUENCE 95 AA; 10804 MW; 77F5CDE879E69FF7 CRC64;

Query Match 73.2%; Score 82; DB 13; Length 95;
Best Local Similarity 77.8%; Pred. No. 4.2e-05; Indels 0; Gaps 0;
Matches 14; Conservative 4; Mismatches 0;

QY 2 LWAAQRYGRELRRMSDEF 19
|||||
Db 38 LWAAQRYGRELRRMSDEF 55

RESULT 6
Q10843
```

Query Match	43.8%	Score 49	DB 2	Length 453
Best Local Similarity	55.6%	Pred. No. 23		
Matches	10	Conservative	4	Mismatches
			2	Indels
			2	Gaps
QY	3	WAAQRYGR--ELRRMSDE	18	
Db	65	WASERQGREELRLASE	82	
RESULT	8			
Q9HZQ3				
ID	Q9HZQ3	PRELIMINARY;	PRT;	1248 AA.
AC	Q9HZQ3;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)		
DE	COBALAMIN BIOSYNTHETIC PROTEIN COBN.			
GN	COBN OR PA2944.			
OS	Pseudomonas aeruginosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas.			
OX	NCBI_TaxID=287;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PA01;			
RX	MEDLINE=20437337; PubMed=10984043;			
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,			
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,			
RA	Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,			
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,			
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,			
RA	Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;			
RT	"Complete genome sequence of Pseudomonas aeruginosa PA01, an			
RT	opportunistic pathogen."			
RL	Nature 406:959-964(2000).			
DR	EMBL; AE004720; AAC06332.1; -			
DR	InterPro; IPR000049; -			
DR	InterPro; IPR000408; -			
DR	ProDom; PD003528; -; 1.			
DR	PROSITE; PS00626; RC01.2; UNKNOWN_1.			
SEQ	SEQUENCE 1248 AA; 138499 MW; C3D3DBFEE6736C7A CRC64;			
Query Match	43.8%	Score 49	DB 2	Length 1248
Best Local Similarity	50.0%	Pred. No. 69		
Matches	11	Conservative	4	Mismatches
			5	Indels
			2	Gaps
QY	2	LWAAQRYG--RELRRMSDEFVD	21	
Db	611	LTRAESYGPLRLERLADEFYD	632	
RESULT	9			
Q9HY62				
ID	Q9HY62	PRELIMINARY;	PRT;	295 AA.
AC	Q9HY62;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last annotation update)		
DE	HYPOTHETICAL PROTEIN PA3555.			
GN	PA3555.			
OS	Pseudomonas aeruginosa.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas.			
OX	NCBI_TaxID=287;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=PA01;			
RX	MEDLINE=20437337; PubMed=10984043;			
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,			
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,			
RA	Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,			
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,			

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA O'Connor L., Strasser A., O'Reilly L

Query Match	41.5%;	Score 46.5;	DB 5;	Length 486;
Best Local Similarity	44.0%;	Pred. NO. 58;		
Matches 11:	Conservative	4:	Mismatches	5:
			Indels	5:
			Gaps	1:

RL Nature 368:32-38(1994).
DR EMBL; 279759; CAB02138.1; -
DR InterPro; IPR001201; -
DR InterPro; IPR002058; -
DR InterPro; IPR002934; -
DR Pfam; PF01909; NTP_transf_2; 1.
SQ SEQUENCE 848 AA; 95038 MW; D4F9DA836DCFD53 CRC64;

Query Match 40.2%; Score 45; DB 5; Length 848;
Best Local Similarity 36.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 WAAQRYGRELRLMSDEFVD 21
| :||| : : :||
Db 43 WRRKRYGLNIQGLHEEIVD 61

Search completed: October 9, 2001, 15:54:57
Job time: 192 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2001, 15:54:03 ; Search time 28.81 Seconds
(without alignments)
55.525 Million cell updates/sec

Title: US-09-580-523-1_COPY_103_123

Perfect score: 112
Sequence: 1 NLWAAQRYGRELRRMSDEFVD 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	91.1	204	2 A55671	bad protein - mous
2	53	47.3	223	2 D70760	hypothetical prote
3	49	43.8	453	2 E83517	conserved hypothet
4	49	43.8	1248	2 G83278	cobalamin biosynth
5	47.5	42.4	595	2 B72801	gp13 protein - Myc
6	47	42.0	295	2 F83201	conserved hypothet
7	46.5	41.5	503	1 CTBPRH	site-specific DNA-
8	45	40.2	287	2 S43852	neuropeptide Pol-R
9	45	40.2	370	2 S38185	2-dehydro-3-deoxyp
10	45	40.2	380	2 I38435	angiotensin recept
11	45	40.2	564	2 H75403	glycosyl hydrolase
12	45	40.2	848	2 T28055	hypothetical prote
13	44	39.3	335	2 T52577	gibberellin 2beta-
14	44	39.3	516	2 A96753	probable threonine
15	44	39.3	1008	2 S55603	DNA polymerase rep
16	43.5	38.4	503	2 JQ1019	site-specific DNA-
17	43	38.4	156	2 C81868	hypothetical prote
18	43	38.4	220	2 F72289	oxidoreductase, so
19	43	38.4	232	1 A64538	cytochrome-c oxida
20	43	38.4	232	2 H71969	cytochrome oxidase
21	43	38.4	325	2 H69829	3'-oxoacyl- acyl-ca
22	43	38.4	463	2 F72853	Acorif-30 protein -
23	43	38.4	472	2 T41775	AcMNPV orf30 - Bom
24	43	38.4	1557	2 T28811	hypothetical prote
25	42	37.5	185	2 H72259	ribosome recycling
26	42	37.5	202	2 D83450	probable cytochrom
27	42	37.5	432	1 D64773	trigger factor lva
28	42	37.5	432	2 F85340	hypothetical prote
29	42	37.5	461	2 B82155	deoxyribodipyrimid

30	42	37.5	526	2 T08545	threonine synthase
31	42	37.5	752	1 KXRTC1	proprotein convert
32	42	37.5	795	2 T05860	alpha,alpa-trehal
33	41.5	37.1	1792	2 T13939	myosin V - fruit f
34	41	36.6	69	2 T44956	70K heat shock cha
35	41	36.6	166	2 T25773	hypothetical prote
36	41	36.6	203	2 B83452	probable cytochrom
37	41	36.6	206	2 E82200	cytochrome c oxida
38	41	36.6	352	2 T12515	hypothetical prote
39	41	36.6	388	2 T22799	hypothetical prote
40	41	36.6	391	1 D64801	probable monooxyge
41	41	36.6	391	2 G85566	hypothetical prote
42	41	36.6	395	2 A82827	conserved hypothet
43	41	36.6	447	2 F85356	hypothetical prote
44	41	36.6	567	2 T33400	protein kinase C h
45	41	36.6	577	2 T40297	membrane transport

ALIGNMENTS

RESULT 1

A55671

bad protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999

C:Accession: A55671

R:Yang, E.; Zha, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.

Cell 80, 285-291, 1995

A>Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promot

A:Reference number: A55671; MUID:95136361

A:Accession: A55671

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-204 <YAN>

A:Cross-references: GB:L37296; NID:g639778; PIDN:AAA64465.1; PID:g639779

C:Keywords: heterodimer

Query Match 91.1%; Score 102; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEF 19

|||||

Db 140 NLWAAQRYGRELRRMSDEF 158

RESULT 2

D70760

hypothetical protein Rv2014 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: D70760

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987

A:Accession: D70760

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-223 <COL>

A:Cross-references: GB:Z74025; GB:AL123456; NID:g3261586; PIDN:CAA98415.1; PID:el2999

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv2014

Query Match 47.3%; Score 53; DB 2; Length 223;
Best Local Similarity 58.8%; Pred. No. 0.83;

C;Species: Mycobacterium phage D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-Jan-2000
C;Accession: B72801
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 29, 143-164, 1998
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.
A;Reference number: A72800; MUID:98300335
A;Accession: B72801
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-595 <FOR>
A;Cross-references: GB:AF022214; NID:g3l72250; PIDN:AAC18453.1; PID:g3l72260
C;Genetics:
A;Gene: 13
C;Superfamily: Mycobacterium phage L5 gene 13 protein

Query Match 42.4%; Score 47.5; DB 2; Length 595;
Best Local Similarity 47.6%; Pred. No.16;
Matches 10; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

Qy 1 NLWAAQRYGRELRRMSDEVD 21
::| | | | |
Db 435 DIWDPKYGGVEVPR---EFVD 452

RESULT 6
F83201
conserved hypothetical protein PA3555 [imported] - Pseudomonas aeruginosa (strain PAO
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83201
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337
A;Accession: F83201
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-295 <STO>
A;Cross-references: GB:AE004776; GB:AE004091; NID:g9949701; PIDN:AAG06943.1; GSPDB:GN
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3555
C;Superfamily: Escherichia coli hypothetical protein b2256

Query Match 42.0%; Score 47; DB 2; Length 295;
Best Local Similarity 40.0%; Pred. No.9.4;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 2 LWAAQRYGRELRRMSDEVD 21
:| | :| | | |
Db 120 VWSVQQLGQIRRGSDCLAD 139

RESULT 7
F83P8H
site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - phage rho-lis
N;Alternate names: DNA cytosine methylase; DNA methyltransferase
C;Species: phage rho-lis
A;Note: host Bacillus subtilis
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 24-Oct-1997
C;Accession: A28137
R;Behrens, B.; Noyer-Weidner, M.; Pawlek, B.; Lauster, R.; Balganesch, T.S.; Trautner,
EMBO J. 6, 1137-1142, 1987
A;Title: Organization of multispecific DNA methyltransferases encoded by temperate Ba
A;Reference number: A91063; MUID:87246516
A;Accession: A28137
A:Molecule type: DNA
A;Residues: 1-475; 'E', 477-503 <BEH>

submitted to the EMBL Data Library, September 1996

A:Reference number: Z20462

A:Accession: T28055

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-848 <WIL>

A:Cross-references: PIDN:CAB02138.1; GSPDB:CN00019; CESP:ZK858.1

A:Experimental source: clone ZK858

C:Genetics:

A:Gene: CESP:ZK858.1

A:Map position: 1

A:Introns: 26/3; 82/3; 130/3; 195/3; 241/3; 613/1; 762/1

```

Query Match      40.2%;      Score 45;      DB 2;      Length 848;
Best Local Similarity 36.8%;      Pred. No. 55;
Matches 7;      Conservative 5;      Mismatches 7;      Indels 0;      Gaps 0;

QY      3      WAAQRYGRELRRMSDEEVD      21
      |      |||      ::      :      |      |
Db      43      WRRKRYGLNIOGLHEEYVD      61

```

gibberellin 2beta-dioxygenase (EC 1.14.11.13) 3 [validated] - Arabidopsis thaliana
N;Alternate names: gibberellin 2-oxygenase; gibberellin 2beta-dioxygenase (EC 1.14.11.1.
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 02-Feb-2001
C;Accession: T52577; A64758
R;Thomas, S.G.; Phillips, A.L.; Hedden, P.
Proc. Natl. Acad. Sci. U.S.A. 96, 4698-4703, 1999
A;Title: Molecular cloning and functional expression of gibberellin 2-oxidases, multi
A;Reference number: Z26123

A>Title: Molecular cloning and functional expression of gibberellin 2-Oxidases, multigene family in Arabidopsis thaliana.
A:Reference number: Z66123
A:Accession: T52577
A:Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-335 <THO>
A:Cross-references: EMBL:AJ132437; PIDN:CABA1009.1
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koob, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487

A:Molecule type: DNA
A:Residues: 1-335 <STO>
A:Cross-references: GB:AE002033; NID:g3128216; PIDN:AAC36696.1; GSPDB:GN00139
C:Genetics:
A:Gene: ga2ox3; At2g34550
A:Map position: 2
C:Function:
A:Description: EC 1.14.11.13 [validated; MUID:99218343]
C:Superfamily: l-aminocyclopropane-1-carboxylate oxidase
C:Keywords: oxidoreductase

```

C;keywords: oxidoreductase

Query Match          39.3%;   Score 44;   DB 2;   Length 335;
Best Local Similarity 38.9%;   Pred. No. 31;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY      4  AAOYRGRELRRMSDEFVD 21
      | : | : | : | : | :
Db      136  AVEEYIKEMRMSSKPLE 153

```

DD 136 AVEEYIKEMRMSSKPLE 153

RESULT 14

A96753

probable threonine synthase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96753
 C:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: A96753
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE005173; NID:g5903070; PIDN:AAD55628.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F3N23.1
 A:Map position: 1

Query Match 39.3%; Score 44; DB 2; Length 516;
Best Local Similarity 40.0%; Pred. No. 48;
Matches 8; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NLWAAQRYGRELRRMSDEFV 20
||:|:|:|:|:|:|:|:|:|
Db 163 NLFWAERFGKQYLQMNDLWV 182

RESULT 15

S55603
DNA polymerase replicative chain - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C:Accession: S55603
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501
A:Accession: S55603
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1008 <TEL>
A:Cross-references: GB:U20824; NID:g695172; PIDN:RAC13796.1; PID:g695181
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
C:Superfamily: herpesvirus DNA-directed DNA polymerase

Query Match 39.3%; Score 44; DB 2; Length 1008;
Best Local Similarity 50.0%; Pred. No. 94;
Matches 11; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

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QY 1 NLWAAQRYG--RELRRMSDEFV 20
      |:| |:| |:| |:| |:|
Db 645 NVWLAKRKAIRRELATVSDAV 666
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Search completed: October 9, 2001, 15:54:04
Job time: 234 sec

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QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLMWAAQRYGRLRMADE 120
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Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLMWAAQRYGRLRMSDE 120
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDRNLGRGSSAPSQ 168
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Db 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||
RESULT 2
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
US-08-985-335-1
Query Match 99.7%; Score 902; DB 3; Length 168;
Best Local Similarity 99.4%; Pred. No. 2.1e-84;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDGPSSGKGHHQAPGLLDASHQOQPTSSSH 60
|||||
Db 1 MFOIPEFEPSEQDSSAERGLGSPAGDGPSSGKGHHQAPGLLDASHQOQPTSSSH 60
|||||
QY 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLMWAAQRYGRLRMADE 120
|||||
Db 61 HCGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLMWAAQRYGRLRMSDE 120
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||

Db 121 FVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDRNLGRGSSAPSQ 168
|||||
RESULT 3
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-665-617-2
Query Match 82.7%; Score 748; DB 1; Length 166;
Best Local Similarity 83.4%; Pred. No. 9e-69;
Matches 146; Conservative 4; Mismatches 9; Indels 16; Gaps 3;
QY 1 MFOIPEFEPSEQDSSAERGLGSPAGDGPSSGKGHHQAPG-----LLWDASHQOE 53
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Db 1 MFOIPEFEPSEQDSSAERG-WRSPAGTGP-----QAPASIIARPQVLWDASHQOE 51
|||||
QY 54 OPTSSSHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRSRAPPNLMWAAQRYGRE 113
|||||
Db 52 OPTSSSHGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPRGRARAPPNLMWAAQRYGRE 111
|||||
QY 114 LRRMADEFVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDRNLGRGSSAPSQ 168
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Db 112 LRRMADEFVDSFKKGLPRPKSAGTATQMROSSWTRVFQSWDRNLGRGTAAPSQ 166
|||||
RESULT 4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7

Query Match 81.9%; Score 741; DB 3; Length 168;
Best Local Similarity 84.5%; Pred. No. 4.7e-68;
Matches 142; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFQIPEPESQEDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHQOEQTSSSH 60
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DB 1 MFQIPEPESQEDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHQOEQTSSSH 60
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QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEPPFRGRSRSPNPNLWAAQRYGRELRRMADE 120
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DB 61 HGGAGCGDPSPQLPRGDDRRDGGGAQPPFRGRSRSPNPNLWAAQRYGRELRRMSDE 120
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QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
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DB 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||

RESULT 5
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."
US-08-333-565-2

Query Match 71.4%; Score 646; DB 1; Length 204;
Best Local Similarity 75.0%; Pred. No. 2.7e-58;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY 1 MFQIPEPESQEDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHQOEQTSSSH 60
|||||
DB 43 MFQIPEPESQEDASATDRLGSLTEDQP---GPY--LAPLLGLSLHQQGRAATNSH 97
|||||
QY 61 HGGAGAVEIRSRHSYPAGTDEDEGMGEPPFRGRSRSPNPNLWAAQRYGRELRRMADE 120
|||||
DB 98 HGGAGAMETRRHSYPAGTEDEGMEEELPFRGRSRSPNPNLWAAQRYGRELRRMSDE 157
|||||
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
|||||
DB 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWWDRNLGKGSTPSQ 204
|||||

RESULT 6
US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565

```

: FILING DATE: 31-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30, 223
: REFERENCE/DOCKET NUMBER: 15726A-000700
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 204 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..204
: OTHER INFORMATION: /note= "Deduced ami
: OTHER INFORMATION: of mouse BAD."
US-08-461-479-2

```

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. NO. 2.7e-58;
Matches 126; Conservative 13; Mismatches 23; Indels 6; Gaps 3;

QY:	1	MFOIPEPSEQEDSSAERGLGSPAGDGPSCSGKHHRQAQCLLWDASHQEQBPQTSSSH	60
Db	43	MFQIPEPSEQEDASATDKGLGSLTEQDQ---GYY--LAPGLGSLNHQOGRAAATNSH	97
QY	61	HGGAGAVETSRHSYYPAGTDEDEGMCEBEPSPFGRSRSAPPNLMAAQRYGRELRMADE	120
Db	98	HGGAGAMETSRHSYYPAGTDEDEGMCEBEPSPFGRSRSAPPNLMAAQRYGRELRMSDE	157
QY	121	FVDSFKKGLPRPSAGTATQMRQSSSWTRVFQSWDNRNLGRGSSAPSQ	168
Db	158	FEGSF-KGLPRPSAGTATQMRQSSAGWTRIIQSWDNRNLKGSTSPQ	204

RESULT 7
US-08-733-505A-1
; Sequence 1, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-733-505A-1

```

Query Match 71.4%; Score 646; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 2.7e-58;
Matches 126; Conservative 13; Mismatches 23. Indels

Qy	1	MFQIPEPESQEEDSSAERGLGSPAGDGPSGGKHHRQAOPGLLWDASHQOQPPTSSSH	60
Dd	43	MFQIPEPESQEEDASATDRGLPSLTEDQP--GPY--LAPGLLGSLNIHQCGRAATNSH	97
Qy	61	HGGAGAVEISRHSYPAGTTEDEGMCEEPSPPFRGRSRSAAPPNLWAAQRYGRELRMADE	120
Dd	98	HGGAGAMETRSHSSYPAGTTEDEGMEEELSPFRGRSRSAAPPNLWAAQRYGRELRMSDE	157
Qy	121	FVDSFKKGLPRPKSACGATQMRQSSSWTRVPFQSWDNRNLCRGSSAPSQ	168
Dd	158	FEGSF-KGLPRPKSAGTQMRSAGWTRIQQSWDRNLKKGSTPQS	204

RESULT 8
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilman
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
Acids and Methods of Use
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

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Query Match      71.3%; Score 645; DB 2; Length 204;
Best Local Similarity 75.0%; Pred. No. 3.4e-58;
Matches 126; Conservative 12; Mismatches 24; Indels 6; Gaps 3;
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Db      43 MFQIPEPEPEQEDASNDRGGLPSLTEDQP---GPY--LAPGLLGSNIHQQGRAATNSH 97
QY      61 HGGAGAVEIRSRHSSYPAGTEDEGMEGEEPSFPRGSRSRAPPNLWAAQRYGRELRRMADE 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      98 HGGAGAMETRSRHSYPAGTEDEGMEEEELSPPFRGSRSRAPPNLWAAQRYGRELRRMTDE 157
QY      121 FVDSFKGLPRPSAGTATOMROSSWTRVFQSWDRNLGRGSSATPSQ 168
      |  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      158 FEGSF-KGLPRPSAGTATOMROSAGWTRIIQSWDRNLGKGGSTPSQ 204

```

RESULT 9
 US-08-733-505A-12
 ; Sequence 12, Application US/087333505A
 ; Patent No. 5856445
 ; GENERAL INFORMATION:
 ; APPLICANT: KORSMEYER, STANLEY J.
 ; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 ; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HOWELL & HAERKAMP, L.C.
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400
 ; CITY: ST. LOUIS
 ; STATE: MISSOURI
 ; COUNTRY: USA
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/733,505A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HOLLAND, DONALD R.
 ; REGISTRATION NUMBER: 35,197
 ; REFERENCE/DOCKET NUMBER: 965458
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 727-5188
 ; TELEFAX: (314) 727-6092
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 204 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-733-505A-12

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Query Match          71.0%; Score 643; DB 2; Length 204;
Best Local Similarity 74.4%; Pred. No. 5.4e-58;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;

QY      1 MFQIPEPESQEEDSSAERCGLGSPAGDPSGSKHHRQA PGLLWDASHQOEQTSSSH 60
        |||||
Db       43 MFQIPEPESQEEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSIHQOGRAATNSH 97
        |||||
QY      61 HGGAGA VEIKRSISSYPAGTDEDDBGMEEPSPFGRGRSRSA PPNLWAAQRYGRELRMADE 120
        |||||
Db       98 HGGAGANETRSHSAYPACTEEDBGMEELSPFGRGRSRSA PPNLWAAQRYGRELRMSDE 157
        |||||
QY      121 FVDSFKKGLPRPKSAGTATOMRQSSSWTRVFQSWMDNLGRGSSAPSQ 168
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Db       158 FEGSF-KGLPRPKSAGTATOMROSAGWTRIIOSWMDNLGRGGSTPSQ 204

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RESULT 10
US-08-733-505A-13
; Sequence 13, Application US/08733505A

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; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-13

Query Match 71.0%; Score 643; DB 2; Length 204;
Best Local Similarity 74.4%; Pred. No. 5.4e-58;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 60

QY 1 MFQIPEPSEQEDSSAERGLGPGSPAGDGPSSGKHHRQAPGLLWDASHHQDEOPTSSSH 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 43 MFQIPEPSEQEDASATDRLGFLTEQDQ---GPY--LAPGLLGSNIHQGRAATNSH 97
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 HGGAGAYEIRSHSSYPAGTDEDEGMGEESPFRGSRSPAPPLNMAAQRYGRELRRMADE 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98 HGGAGAMETRSRHSYPAGTDEDEGMEELSPFRGSRAPPLNMAAQRYGRELRRMSDE 157
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 FVDSFKGLPRPKSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168
   | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWDRNLGKGSTPSQ 204
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 70.7%; Score 640; DB 2; Length 204;
Best Local Similarity 73.8%; Pred. No. 1.1e-57;
Matches 124; Conservative 15; Mismatches 23; Indels 6; Gaps 3;
QY 1 MFQIPEFSEQEDSSAERGLPGSPAGDPGSGKHHKQAPGLLDASHQEQPTSSSH 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 43 MFQIPEFSEQEDASATDGLGSLTEDQP---GPY--LAPGLLGSNIHQOQRAATNSH 97
QY 61 HGGAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 98 HGGAGAVEIRSRHSSYPAGTDEDEGMGEELSPFRGRSRAPPNLWAAQRYGRELRRMSDE 157
QY 121 FVDFKKGKLPKPSAGTATQMRQSSSWTRVFQSWDRNLGRGSSAPSQ 168
| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 158 FEGSGF-KGLPRKPSAGTATQMRQSQSGATWTRIIQSWDRNLGKGGSTPSQ 204

RESULT 12
US-08-733-505A-55
Sequence 55, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-55

Query Match 34.4%; Score 311; DB 2; Length 59;
Best Local Similarity 98.3%; Pred. No. 5.7e-25;
Matches 58; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADEF 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

RESULT 13
US-08-733-505A-56
Sequence 56, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-56

Query Match 34.0%; Score 308; DB 2; Length 59;
Best Local Similarity 96.6%; Pred. No. 1.1e-24;
Matches 57; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADEF 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

RESULT 14
US-08-733-505A-57

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; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-57

Query Match 34.0%; Score 308; DB 2; Length 59;
Best Local Similarity 96.6%; Pred. No. 1.le-24;
Matches 57; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADEF 121
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

RESULT 15
US-08-733-505A-58
; Sequence 58, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733,505A
; FILING DATE:

; Sequence 57, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-733-505A-58

Query Match 33.7%; Score 305; DB 2; Length 59;
Best Local Similarity 94.9%; Pred. No. 2.3e-24;
Matches 56; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 63 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMADEF 121
Db 1 GAGAVEIRSRHSSYPAGTDEDEGMGEPPSPFRGRSRAPPNLWAAQRYGRELRRMSDEF 59

Search completed: October 9, 2001, 15:58:34
Job time: 59 sec
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RESULT 7
US-08-733-505A-1
; Sequence 1, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733.505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELEPHONE: (314) 727-5188
; FAX: (314) 727-6092
; TELEPHONE FOR SEQ ID NO: 1:

QY 1 MFQIPFEPSEQEDSSAERGLPGSPAGDGPSCGSKHHRQAPELLWDASHHQEQPTSSSH 60
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Query Match      71.0%; Score 643; DB 2; Length 204;
Best Local Similarity 74.4%; Pred. NO. 5.4e-58;
Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps 3;

1  MQIPEFSEQEDSSAERGLGSPAGDCPGSCGKHRRQAPGLLWDASHQOQPPTSSSH 60
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43  MQIPEFSEQEDASATORGLPSTEDQP---GPY--LAPLLGSNIHQQGRAATNSH 97
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61  HGCAGAVETRSHSSYPACTEEDGEGEPPSPRGRSRSAPPNLWAAQRYGRELRRMADE 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
98  HGCAGAVETRSHSAYPACTEEDGEGEELSPPRGRSRSAPPNLWAAQRYGRELRRMSDE 157
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWWDRNLGRGSAPSQ 168
   || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
158 FEGSF-KGLPRPKSAGTATQMRQSGAGWTRIIQSWWDRNLCKGGSTPSQ 204
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
US-08-733-505A-13
; Sequence 13, Application US/087333505A

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```

; Patent No. 5856445
;
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733.505A
; FILING DATE:
;
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-733-505A-13
;
; Query Match 71.0%; Score 643; DB 2; Length 204;
; Best Local Similarity 74.4%; Pred.No. 5.4e-58;
; Matches 125; Conservative 14; Mismatches 23; Indels 6; Gaps
;
; 1 MFOIPEFPSEQEDSSSAERGLGSPAGDPGSGSKHHRQAPGLLWDASHHQEQPTSSSH 60
; ||||| ||||| ||||| : ||||| | : ||||| ||| : :||
; 43 MFOIPEFPSEQEDASATDRGLGPSLTEDQP---GPY--LAPGLLGSNIHQGRATNSH 97
; ||||| ||||| ||||| : ||||| | : ||||| ||| : :||
; 61 HGGAGAVEIRSRHSSYPAGTDEDCMGEEPPSPFRGSRSAAPNLWAAORYGRELRRMADE 120
; ||||| : ||||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||
; 98 HGGAGAMETRSRHSYPAGTDEDCMGEEELSPFRGSRRAAPPNLWAAORYGRELRRMSDE 157
; ||||| : ||||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||
; 121 FVDSFKGLPRPKSAGTATQMRQSSWTRVFQSWDRNLGRGSSAPSQ 168
; | || ||||| ||||| ||||| : ||||| : ||||| : ||||| : ||||| : |||||
; 158 FRGSP-KGLPRPKSAGTATQMRQSGAWTRIIQSWDRNLGKGSPSQ 204
; ||||| : ||||| ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||
;
; RESULT 11
; US-08-733-505A-14
; Sequence 14, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
;
; COMPUTER READABLE FORM:

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:34 ; Search time 18.99 Seconds
(without alignments)
182.158 Million cell updates/sec

Title: 09-580523-lb
Perfect score: 905
Sequence: 1 MFQIPEPESQEDSSAER.....RVFQSWDRNLGRSSAFSQ 168

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	99.7	168	2	US-08-717-123-2
2	902	99.7	168	3	US-08-985-335-1
3	748	82.7	166	1	US-08-665-617-2
4	741	81.9	168	3	US-08-985-335-7
5	646	71.4	204	1	US-08-333-565-2
6	646	71.4	204	2	US-08-661-479-2
7	645	71.4	204	2	US-08-733-505A-1
8	645	71.3	204	2	US-08-717-123-3
9	643	71.0	204	2	US-08-733-505A-12
10	643	71.0	204	2	US-08-733-505A-13
11	640	70.7	204	2	US-08-733-505A-14
12	311	34.4	59	2	US-08-733-505A-55
13	308	34.0	59	2	US-08-733-505A-56
14	308	34.0	59	2	US-08-733-505A-57
15	305	33.7	59	2	US-08-733-505A-58
16	113	12.5	23	1	US-08-333-565-10
17	113	12.5	23	2	US-08-661-479-10
18	97	10.7	2509	2	US-08-149-097D-35
19	96.5	10.7	1182	4	US-09-041-886-21
20	90.5	10.0	393	2	US-09-026-587-3
21	90.5	10.0	393	2	US-09-227-420-3
22	90	9.9	434	1	US-08-337-602-3
23	90	9.9	434	3	US-08-558-135-3
24	90	9.9	2237	1	US-08-455-543A-48
25	90	9.9	2237	2	US-08-223-305C-48
26	90	9.9	2337	3	US-08-713-118-2
27	90	9.9	2337	4	US-09-452-007-2

28 90 9.9 2339 1 US-08-455-543A-47 Sequence 47, Appl
29 90 9.9 2339 2 US-08-223-305C-47 Sequence 47, Appl
30 89 9.8 418 2 US-09-026-587-1 Sequence 1, Appl
31 89 9.8 418 2 US-09-227-420-1 Sequence 1, Appl
32 87 9.6 575 3 US-08-922-865-2 Sequence 2, Appl
33 85.5 9.4 378 2 US-08-986-217-6 Sequence 6, Appl
34 85.5 9.4 1159 3 US-08-956-242-13 Sequence 13, Appl
35 85.5 9.4 1159 3 US-09-351-215-13 Sequence 13, Appl
36 85.5 9.4 1159 4 US-09-226-012-2 Sequence 2, Appl
37 85.5 9.4 1159 4 US-09-226-012-4 Sequence 4, Appl
38 84 9.3 16 1 US-08-333-565-17 Sequence 17, Appl
39 84 9.3 16 2 US-08-661-479-17 Sequence 17, Appl
40 84 9.3 380 2 US-09-026-587-4 Sequence 4, Appl
41 84 9.3 380 2 US-09-227-420-4 Sequence 4, Appl
42 83 9.2 16 1 US-08-333-565-26 Sequence 26, Appl
43 83 9.2 16 2 US-08-661-479-26 Sequence 26, Appl
44 83 9.2 591 3 US-09-082-737-2 Sequence 2, Appl
45 83 9.2 696 3 US-08-906-865-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match 99.7%; Score 902; DB 2; Length 168;
Best Local Similarity 99.4%; Pred. No. 2.1e-84;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFQIPEPESQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHHQEQPTSSSH 60
Db 1 MFQIPEPESQEDSSAERGLGSPAGDPSGSGKHRRQAPGLLWDASHHQEQPTSSSH 60

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QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
 Db 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
 QY 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
 Db 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 2
 US-08-985-335-1
 ; Sequence 1, Application US/08985335
 ; Patent No. 6080847
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 ; TITLE OF INVENTION: PROLIFERATION
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/985.335
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0421 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SYNORAB01
 CLONE: 358673

US-08-985-335-1
 Query Match 99.7%; Score 902; DB 3; Length 168;
 Best Local Similarity 99.4%; Pred. No. 2,1e-84;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQOEQPTSSSH 60
 Db 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQOEQPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
 Db 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120

US-08-985-335-1
 Query Match 99.7%; Score 902; DB 3; Length 168;
 Best Local Similarity 99.4%; Pred. No. 2,1e-84;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQOEQPTSSSH 60
 Db 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPGLLDASHQOEQPTSSSH 60
 QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
 Db 61 HGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120

US-08-985-335-1
 Query Match 99.7%; Score 902; DB 3; Length 168;
 Best Local Similarity 99.4%; Pred. No. 2,1e-84;
 Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 121 FVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 3
 US-08-665-617-2
 ; Sequence 2, Application US/08665617
 ; Patent No. 5663316
 ; GENERAL INFORMATION:
 ; APPLICANT: Xudong, Yin
 ; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville
 ; STATE: Florida
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/665,617
 ; FILING DATE:
 ; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: CL-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-617-2

Query Match 82.7%; Score 748; DB 1; Length 166;
 Best Local Similarity 83.4%; Pred. No. 9e-69;
 Matches 146; Conservative 4; Mismatches 9; Indels 16; Gaps 3;

QY 1 MFOIPEFEPSEQEDSSAERGLGSPAGDGPSCGKHHRQAPG-----LLWDASHQOE 53
 Db 1 MFOIPEFEPSEQEDSSAERG-WRSPAGTGP-----QAPASIIARQVLDASHQOE 51
 QY 54 OPTSSSHGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGRSRAPPNLWAAQRYGRE 113
 Db 52 OPTSSSHGGAGAVEIRSRHSSYPAGTDEGMEGEPSPFRGARARPPPNLWAAQRYGRE 111
 QY 114 LRRMADEFVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGSSAPSQ 168
 Db 112 LRRMADEFVDSFKKGLPRKSGATATQMRQSSSWTRVFQSWWDRNLGRGTAAPSQ 166

RESULT 4
 US-08-985-335-7
 ; Sequence 7, Application US/08985335
 ; Patent No. 6080847
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 ; TITLE OF INVENTION: PROLIFERATION

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 9, 2001, 15:58:34 ; Search time 18.99 Seconds
(without alignments)
182.158 Million cell updates/sec

Title: 09-580523-lb

Perfect score: 905

Sequence: 1 MFQIPEPESQEDSSAER.....RVFQSWDRNLGRSSAPSQ 168

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

tal number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
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 - 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/2/1aa/PTCUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	902	99.7	168	2	US-08-717-123-2
2	902	99.7	168	3	US-08-985-333-1
3	748	82.7	166	1	US-08-665-617-2
4	741	81.9	168	3	US-08-985-333-7
5	646	71.4	204	1	US-08-333-565-2
6	646	71.4	204	2	US-08-661-479-2
7	646	71.4	204	2	US-08-733-505A-1
8	645	71.3	204	2	US-08-717-123-3
9	643	71.0	204	2	US-08-733-505A-12
10	643	71.0	204	2	US-08-733-505A-13
11	640	70.7	204	2	US-08-733-505A-14
12	311	34.4	59	2	US-08-733-505A-55
13	308	34.0	59	2	US-08-733-505A-56
14	308	34.0	59	2	US-08-733-505A-57
15	305	33.7	59	2	US-08-733-505A-58
16	113	12.5	23	1	US-08-333-565-10
17	113	12.5	23	2	US-08-661-479-10
18	97	10.7	2509	2	US-08-149-097D-35
19	96.5	10.7	1182	4	US-09-041-886-21
20	90.5	10.0	393	2	US-09-026-587-3
21	90.5	10.0	393	2	US-09-227-420-3
22	90	9.9	434	1	US-08-337-602-3
23	90	9.9	434	3	US-08-558-135-3
24	90	9.9	2237	1	US-08-455-543A-48
25	90	9.9	2237	2	US-08-223-305C-48
26	90	9.9	2237	3	US-08-713-118-2
27	90	9.9	2237	4	US-09-452-007-2

28	90	9.9	2339	1	US-08-455-543A-47	Sequence 47, Appl
29	90	9.9	2339	2	US-08-223-305C-47	Sequence 47, Appl
30	89	9.8	418	2	US-09-026-587-1	Sequence 1, Appli
31	89	9.8	418	2	US-09-227-420-1	Sequence 1, Appli
32	87	9.6	575	3	US-08-322-865-2	Sequence 2, Appli
33	85.5	9.4	378	2	US-08-986-217-6	Sequence 6, Appli
34	85.5	9.4	1159	3	US-08-956-242-13	Sequence 13, Appl
35	85.5	9.4	1159	3	US-09-351-215-13	Sequence 13, Appl
36	85.5	9.4	1159	4	US-09-226-012-2	Sequence 2, Appli
37	85.5	9.4	1159	4	US-09-226-012-4	Sequence 4, Appli
38	84	9.3	16	1	US-08-333-565-17	Sequence 17, Appl
39	84	9.3	16	2	US-08-661-479-17	Sequence 17, Appl
40	84	9.3	380	2	US-09-026-587-4	Sequence 4, Appli
41	84	9.3	380	2	US-09-227-420-4	Sequence 4, Appli
42	83	9.2	16	1	US-08-333-565-26	Sequence 26, Appl
43	83	9.2	16	2	US-08-661-479-26	Sequence 26, Appl
44	83	9.2	591	3	US-09-082-737-2	Sequence 2, Appli
45	83	9.2	696	3	US-08-906-865-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-717-123-2
; Sequence 2, Application US/08717123
; Patent No. 5965703
; GENERAL INFORMATION:
; APPLICANT: Horne, William A.
; APPLICANT: Oltersdorf, Tilman
; TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
; TITLE OF INVENTION: Acids and Methods of Use
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,123
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-717-123-2

Query Match 99.7%; Score 902; DB 2; Length 168;
Best Local Similarity 99.4%; Pred. No. 2.1e-84;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFQIPEPESQEDSSAERGLGSPAGDPSGSGKHHRRQAPGLLDASHOOEPTSSSH 60

DB 1 MFQIPEPESQEDSSAERGLGSPAGDPSGSGKHHRRQAPGLLDASHOOEPTSSSH 60

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QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
DB 61 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120
QY 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168
DB 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168
RESULT 2
US-08-985-335-1
; Sequence 1, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,335
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0535
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 358673
; US-08-985-335-1

Query Match 99.7%; Score 902; DB 3; Length 168;
Best Local Similarity 99.4%; Pred. No. 2.1e-84;
Matches 167; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFQIPEFPEPSEQDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHOQEQPTSSSH 60
DB 1 MFQIPEFPEPSEQDSSAERGLGSPAGDGPSSGKHHQAPGLLDASHOQEQPTSSSH 60
QY 61 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMADE 120
DB 61 HGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRYGRELRRMSDE 120
FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168

Db 121 FVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168

RESULT 3
US-08-665-617-2
; Sequence 2, Application US/08665617
; Patent No. 5663316
; GENERAL INFORMATION:
; APPLICANT: Xudong, Yin
; TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,617
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: CL-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-617-2

Query Match 82.7%; Score 748; DB 1; Length 166;
Best Local Similarity 83.4%; Pred. No. 9e-69;
Matches 146; Conservative 4; Mismatches 9; Indels 16; Gaps 3;
QY 1 MFQIPEFPEPSEQDSSAERGLGSPAGDGPSSGKHHQAPG-----LLWDASHOQE 53
DB 1 MFQIPEFPEPSEQDSSAERG-WRSPAGTGP-----QAPASIIARPOVLWDASHOQE 51
QY 54 OPTSSHHGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRYG 113
DB 52 OPTSSHHGGAGAVEIRSRHSSYPAGTDEGMEEPSPFRGRSRAPPNLWAAQRYG 111
QY 114 LRRMADEFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGSSAPSQ 168
DB 112 LRRMADEFVDSFKKGLPRPKSAGTATQMRQSSWTRVFQSWMDNLGRGTAAPSQ 166

RESULT 4
US-08-985-335-7
; Sequence 7, Application US/08985335
; Patent No. 6080847
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; PROLIFERATION

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GENERAL INFORMATION:

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Query Match      100.0%  Score 145;  DB 18;  Length 168;
Best Local Similarity 100.0%;  Pred. No. 1.6e-11;
Matches 26;  Conservative 0;  Mismatches 0;  Indels 0

QY  1  QSSWTRVFQSWDRNLGRGSSAPSQ  26
      | | | | | | | | | | | | | | | | | |
Db   143 QSSWTRVFQSWDRNLGRGSSAPSQ  168

RESULT 6
US-09-410-372-7

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; Sequence 7, Application US/09410372
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
; TITLE OF INVENTION: PROLIFERATION
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/410,372
; APPLICATION NUMBER: US/09/410,372
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,335
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0421 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 168 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1683637
US-09-410-372-7

Query Match 100.0%; Score 145; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26
Db 143 QSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 7
US-09-456-357-32
; Sequence 32, Application US/09456357
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; TITLE OF INVENTION: METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/09/456,357
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: 60/134,416
; EARLIER FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: 09/087,195
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/378,507
; EARLIER FILING DATE: 1995-01-26
; EARLIER APPLICATION NUMBER: 08/250,478

; EARLIER FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-357-32

Query Match 100.0%; Score 145; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26
Db 143 QSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 8
US-09-580-523-1
; Sequence 1, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-580-523-1

Query Match 100.0%; Score 145; DB 19; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSSWTRVFQSWWDRNLGRGSSAPSQ 26
Db 143 QSSWTRVFQSWWDRNLGRGSSAPSQ 168

RESULT 9
US-09-587-473-21
; Sequence 21, Application US/09587473
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Tsvetkov, Lyuben
; TITLE OF INVENTION: Protein Knockout Technology
; FILE REFERENCE: 44574-5047-WO
; CURRENT APPLICATION NUMBER: US/09/587,473
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 60/137,494
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-587-473-21

Query Match 100.0%; Score 145; DB 19; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QSSSWTRVFQSWDRNLGRGSSAPSQ	26
Db	143	QSSSWTRVFQSWDRNLGRGSSAPSQ	168

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RESULT 10
PCT-US00-11864-3
; Sequence 3, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS
; TITLE OF INVENTION: AND METHODS OF MAKING
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-3

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RESULT 11
US-09-580-523-3
; Sequence 3, Application US/09580523
; GENERAL INFORMATION:
; APPLICANT: Zhou, Xiao-Mai
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS,
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: A7483
; CURRENT APPLICATION NUMBER: US/09/580,523
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 3
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-580-523-3

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RESULT 12
PCT-US00-11864-2
; Sequence 2, Application PC/TUS0011864
; GENERAL INFORMATION:
; APPLICANT: APOPTOSIS TECHNOLOGY, INC.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR REGULATING APOPTOSIS.
; TITLE OF INVENTION: AND METHODS OF MAKING AND SCREENING FOR COMPOUNDS
; TITLE-OF INVENTION: THAT REGULATE APOPTOSIS
; FILE REFERENCE: F137122
; CURRENT APPLICATION NUMBER: PCT/US00/11864

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; CURRENT FILING DATE: 2000-05-30
;
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 204
;
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US00-11864-2

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RESULT 13
PCT-US97-15871-1
; Sequence 1, Application PC/TUS9715871
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-X1/BCL-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/15871
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-15871-1

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RESULT 14
PCT-US97-15871A-1
: Sequence 1. Application PC/TUS9715871A

GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J
; TITLE OF INVENTION: MODULATION OF APOPTOSIS BY SERINE
; TITLE OF INVENTION: PHOSPHORYLATION OF BCL-XL/BCL-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/15871A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-1938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-15871A-1

Query Match 82.8%; Score 120; DB 1; Length 204;
Best Local Similarity 73.1%; Pred. No. 4.7e-08;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
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Db 179 QSAGWTRIIQSWWDRNLGKGSTPSQ 204

RESULT 15
PCT-US98-19765-41
; Sequence 41, Application PC/TUS9819765
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON UNIVERSITY
; TITLE OF INVENTION: CELL DEATH AGONISTS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/19765
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HENDERSON, MELODIE W

REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US98-19765-41

Query Match 82.8%; Score 120; DB 1; Length 204;
Best Local Similarity 73.1%; Pred. No. 4.7e-08;
Matches 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QSSSWTRVFQSWWDRNLGRGSSAPSQ 26
||: ||: ||||| ||||| |||||
Db 179 QSAGWTRIIQSWWDRNLGKGSTPSQ 204

Search completed: October 9, 2001, 16:07:48
Job time: 498 sec

